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Maximum Match 100%
Listing first 45 summaries
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4: pir4:*
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 GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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                                                 histone H1 homolog
histone H1, gonada
1-acylglycerol-3-p
asparaginyl-trna s
hypothetical prote
probable NLP/P60 f
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probable DNA topoi
histone H1 - trout
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Query Match 46.0%; Score 98; DB 2; Le Best Local Similarity 65.3%; Pred. No. 0.028; Matches 32; Conservative 2; Mismatches 9;	RESULT 2 P90725 C;Species: Escherichia coli C;Species: Escherichia coli (strain Ol C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul- C;Accession: F90725 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoya: gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinaga NAR Res. 8, 11-22, 2001 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli A;Reference number: A99629; MUID:21158231; PMID:11258796 A;Accession: F90725 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-394 <hay> A;Gross-references: GB:BA000007; PIDN:BAB34197.1; PID:g13360233; GSPDB:/ A;Gene: ECs0774</hay>	RESULT 1 A25550 A25550 C;Species: Lytechinus pictus (painted urchin) C;Oate: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_C;Accession: A25550 R;Knowles, J.A.; Childs, G.J. Nucleic Acids Res. 14, 8121-8133, 1986 A;Title: Comparison of the late H1 histone genes of the se A;Reference number: A25550, MUID:87040778; PMID:3022245 A;Accession: A25550 A;Mclecule type: DNA A;Residues: 1-210 <kno> A;Cross-references: GB:X04488; NID:99616; PIDN:CAA28177.1;C;Superfamily: histone H1 C;Keywords: chromosomal protein; DNA binding; nucleosome; Query Match Best Local Similarity 65.1%; Pred. No. 0.0053; Matches 28; Conservative 3; Mismatches 11; Ind Qy 1 AKKYAKKAKAKAEK-AKKAYKAAEKKAAKKPAAKKAAKKPAAKKAA</kno>	ALIGNMENTS	30 79 37.1 347 2 A81794 31 78 36.6 217 2 S29309 32 78 36.6 231 2 S5989 33 78 36.6 287 2 S45662 34 78 36.6 309 2 G83013 35 77.5 36.4 376 2 AG0592 36 77 36.2 220 2 A28456 37 77 36.2 220 1 S51660 38 77 36.2 226 1 S51660 38 77 36.2 226 1 S51645 39 77 36.2 229 2 I51227 41 76 35.7 229 2 I51227 41 76 35.7 241 2 JN0748 42 75.5 35.4 220 2 JCS554 43 75.5 35.4 220 2 JCS554 44 75.5 35.4 224 2 T06636 45 75 35.4 224 2 T06636
ingth 394; Indels 6; Gaps 3;	rrichia coli (strain O157:H7, substrain 1 #text_change 18-Jul-2001 K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Hattori, M.; Shinagawa, H. hagic Escherichia coli O157:H7 and geno. 1258796 PID:g13360233; GSPDB:GN00154 RIMD 0509952	tt_change 23-Jul-1999 Bea urchins Lytechinus pictus an '.1; PID:g9617 Be; nucleus Length 210; Indels 1; Gaps 1; AA 208		probable rotamase hypothetical prote histone H1 - Chlam histone H1 - tomat polyhydroxyalkanoa tolA protein [impo histone H1.10 - ch histone H1.5 [vali invariant surface probable transfers histone H1A - Afri histone H1A - Afri histone H1A - impor ribosomal protein hypothetical prote histone H1 - mouse

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KKAAEKAAAEKAAADKKAAAEKAAADKKAAA-AKAAAEKAAAAKAAAEA 267

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C;Species: Escherichia coli
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 01-Mar-2002
C;Accession: JV0057; B64810
R;Levengood, S.K.; Webster, R.E.
J. Bacteriol. 171, 6600-6609, 1989
A;Reference nucleotide sequences of the tolA and tolB genes and localization o A;Reference number: JV0057; MUID:90078104; PMID:2687247
A;Accession: JV0057
                                                                                                C;Keywords: nucleotide binding; P-loop; transmembrane F;14-34/Domain: transmembrane #status predicted <MSS>F;78-301/Domain: helical #status predicted <HSR>F;355-362/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE000177; GB:U00096; NID:g1786955; PIDN:AAC73833.1; PID:g1786960. A;Experimental source: strain K-12, substrain MG1655 C;Comment: tolA and tolB proteins are necessary for colicins E2, E3, A, and K to reach 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: the authors translated the initiation codon GTG for residue 1 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, A.; Rose, D.J.; Mau, B.; Shao, Y.
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A;Residues: 1-394 <STO>
A;Cross-references: GB.AE005174; NID:g12513672; PIDN:AAG55075.1;
A;Experimental source: strain O157:H7, substrain EDL933
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A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    membrane spanning protein TolA [imported] - Escherichia coli (strain O157:FC;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Nov-2001 C;Accession: G85576
                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: B64810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-421 <LEV>
A; Residues: 1-421 <LEV>
A; Cross-references: GB.M28232; NID:g148018; PIDN:AAA24683.1; PID:g148019
A; Experimental source: strain JM105
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D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; We A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1317
                                                                                                                                                                                                                                                                                                                                                                     A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simose, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species. A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Dominguez-Bernal, G.; Duchaud, B.; Durand, L.; Dussurget, O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein homolog lin2055 [imported] - Listeria innocua (strain Clip11262) C;Species: Listeria innocua (c;Species: Listeria innocua (c;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C;Accession: AE1889
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A; Residues: 1-243 <GLA>
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A; Residues: 1-239 <GLA>
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.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feihi,
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;Experimental source: strain Clip11262
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                                                                    AKKYA-KKAKAEKAKKAYKAAEAKKA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ККҮАККАКАЕКАКК---АҮКААБАКК--ААКҮЕКАААЕКАЛАКБААҮБ 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKAAEKAAAEKAAADKKAAAEKAAADKKAAA-AKAAAEKAAAAKAAAEA
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                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.48;
                                                                                                                                                      45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 94.5; DB
Pred. No. 0.04;
7; Mismatches
                                                                                                                                    Score 90; DB 2
Pred. No. 0.11;
3; Mismatches
                                                                                                                                                                             2
                                                                                                                                      11;
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                                                                                                                                                                               Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                             -- AKYEKAAAEKAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F.; Berche, P.; Entian, K.D.;
                                                                                                                                      22;
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                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Maitournam, A.; Ma
Voss, H.; Wehland,
                                                    165
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Feihi, H.
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Fsihi, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        m, A.; Ma
Wehland,
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166

DKAAKE 171

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R;Neesen, J.; Padmanabhan, S.; Buenemann, H.
Eur. J. Blochem. 225, 1089-1055, 1948
A;Title: Tandemly arranged repeats of a novel highly charged
lpha-helical rods within the extremely elongated spermatozoa
A;Reference number: S51364; MUID:95045538; PMID:7957199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Cell. Biol. 8, 1842-1844, 1988
A;Title: Characterization of the structure and transcriptional
A;Reference number: A28100; MUID:88246461; PMID:2837660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-163,'E',164-236,'Q',237-254,257-320,'E',321-1390 <NEW>
A;Cross-references: EMBL:X73481; NID:g313201; PID:g313202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X73481
R;Neesen, J.; Heinlein, U.A.O.; Buenemann, H.
submitted to the EMBL Data Library, June 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Drosophila hydei
C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C;Accession: S51364; S34154
                        R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                            probable hup8 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: G70673
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C; Superfamily: histone H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-211 <LAI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: S34153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S51364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sperm tail-specific protein mst101(2) - fruit fly (Drosophila hydei)
                                                                                                                                                                                                                                                               RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: A28100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     histone H1-beta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: FlyBase:FBgn0011816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      istone H1-beta, embryonic - sea urchin (Strongylocentrotus purpuratus)
;Species: Strongylocentrotus purpuratus (purple urchin)
;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 23-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Accession: A28100
;Lai, Z.C.; Childs, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     662
                                                                                                                                                                                                                                                                                                                                              139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosomal protein; DNA binding; embryo; nucleosome; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-1390 <NEE>
                                                                                                                                                                                                                                                                                                                                                                   h 42.3%;
Similarity 57.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                           SKKTTKKVKKPAAKKAKKPA-AKKAAK--KPAAKKPAAKKAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KETAEKKKCEKAAKKRKEAAEKKKCAEAAKKEKEAAEKKKCEEAA 706
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
Sulston, J.E.; Taylor, K.; Whitehead,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 89.5; DB 2; Length 211; Pred. No. 0.11; 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 90; DB 2;
Pred. No. 0.41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 1390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Indels
S.; Barrell, B.G
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                                                                                                    Gordon,
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Matches

Local Similarity

Conservative

6

Mismatches

13,

Indels

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Gaps

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A; Molecule type: DNA A; Residues: 1-384 <YEL> A; Residues: 1-384 <YEL> A; Residues: 1-384 <YEL> A; Cross-references: GB: M58563; NID: g155066; PIDN: AAA27480.1; PID: g155067 A; Note: the authors translated the codon TTC for residue 316 as Tyr, and C; Keywords: membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, n, J.; Ermolaeva, Milte, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
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C;Superfamily: histone H1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230 A;Accession: G70673
                                                                                                                                                                                                                                                                                                                                                               R;Yelton, D.B.; Limberger, R.J.; Curci, K.; Malinosky-Rummell, F.; Slivienski, Infect. Immun. 59, 3685-3693, 1991
A;Title: Treponema phagedenis encodes and expresses homologs of the Treponema phagedenis encodes e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
B43592
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C;Superfamily: bacterial type I DNA topoisomerase
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A;Residues: 1-899 <STO>
A;Cross-references: GB:AE005673; NID:g13423998; PIDN:AAK24422.1; GSPDB:GN00148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Treponema phagedenis
C;Date: 30-Jan-1993 #sequence_revision
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A;Accession: B87553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-214 < COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                              A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           outer membrane protein TmpB - Treponema phagedenis
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Matches
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;Date: 20-Apr_2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
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                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKKPAKKAAATKSKAKAESDAPAKKTAA-KKPAAKKPAAKKAAPKA 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        АККУАККАКАЕКАК-КАУКААЕАККААКУЕКАААЕКАААКЕААУЕА 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AKKVAKKAPAKKATKAAKKAATKAPA---RKAATKAPAKKAATKA
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40.6%;
54.5%;
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55.6%;
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Score 86.5; DB 2; Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 88;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 89.5; DB Pred. No. 0.11;
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                                      Length 384;
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                                                                                                                                                        residue
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RESULT 13
S34153
                                                                        TolA protein PA0971 [imported] - Pseudomonas aeruginosa (strain PA01) C;Species: Pseudomonas aeruginosa C;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authbors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: F70742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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C;Accession: E83525
R;Stover, C.K.; Pham, X.Q.; Erwin, adman, S.; Yuan, Y.; Brody, L.L.; (
.; Lory, S.; Olson, M.V.
                                                                                                                                               RESULT 14
E83525
                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references:
C;Superfamily: neuro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Neesen, J.; Heinlein, U.A.O.; Buenemann, H. submitted to the EMBL Data Library, June 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mst101-1 protein - fruit fly (Drosophila hydei)
C;Species: Drosophila hydei
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: FlyBase:Dhyd/mst101
                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Genetics:
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A;Accession: S34153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-344 < NEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
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                                                                                                                                                                                                                              KEAAEKKKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEKKKCAEAA 113
                                                                                                                                                                                                                                                        KKAAPAKKAAPAKKAAPAKKAAAKKAPAKKAA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AKEKAAKEKAAKDKAAKEKAAKEKAAK-DKAAKEKAAKE 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYE
                                                                                                                                                                                                                                                                                                                                                                                           nces: FlyBase:FBgn0011816
neurofilament triplet H
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Pred. No. 0.21;
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Pred. No.
                     Coulter,
                                          A.L.;
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                     Mizoguchi, r, S.N.; Fo
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                   hi, S.D.; Warrener, Folger, K.R.; Kas,
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                     M.J.; Br
K.; Lim,
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Search completed:

January 12 secs

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RESULT 15
S61926
                                                                                                                                                                                                                                                                                      A;Title: A novel chromatin-forming histone H1 homologue is encoded by a dispensable and A;Reference number: S61926; MUID:95319329; PMID:7596289
A;Accession: S61926
                                                                                                                                                                                                                                                                                                                                                                          C;Date: 23-Jul-1996 #sequence_revision 06-Sep-1996 #text_change 24-Nov-1999 C;Accession: S61926; S69327
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                              S
                                                                                                                                    C; Superfamily: histone H1
                                                                                                                                                      A;Gene:
                                                                                                                                                                                  A; Molecule type: protein A; Residues: 'X', 3-39 < SCA2>
                                                                                                                                                                                                                    A;Cross-references: EMBL:L37438;
A;Accession: S69327
                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-182 < SCA1>
                                                                                                                                                                                                                                                                                                                                                              R;Scarlato,
                                                                                                                                                                                                                                                                                                                                                                                                              histone H1 homolog - Bordetella pertussis C/Species: Bordetella pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  당
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-347 <570-8
A;Cross-references: GB:AE004530; GB:AE004091; NID:g9946865; PIDN:AAG04360.1; GSPDB:GN001
A;Experimental source: strain PAO1
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Matches
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Microbiol. 15, 871-881,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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58
                                                          39.9%;
il Similarity 61.4%;
27; Conservation
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24; Conser
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.4%;
                                                                                                                                                                                                                                      NID:g777717; PIDN:AAB59120.1; PID:g777718
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                                                                4; Mismatches
                                                                                  Score 85; DB 2
Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 86; DB 2;
Pred. No. 0.33;
6; Mismatches 1
                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                              S.; Manetti,
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Listing first 45 summaries
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 80
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DBH_MYCSM
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RS16_COREP
HBHA_MYCTU
MST1_DROHY
TOLA_PSEAE
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P15869 strongyloce
P95109 mycobacteri
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ALIGNMENTS

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1 AKKYAKKAKAEK-AKKAYKAAEAKKAAKYEKAAAEKAAAKEAA 42 	Query Match 48.6%; Score 103.5; DB 1; Length 210; Best Local Similarity 65.1%; Pred. No. 0.0011; Matches 28; Conservative 3; Mismatches 11; Indels 1; Gaps 1;	EMBL; X04488; CAA28177.1; PIR; A25550; A25550. HSSP; P02259; 1HST. InterPro; IPR005818; Histone H1/H5. InterPro; IPR005819; Histone H5. InterPro; IPR00519; Linkerhist N. Pfam; PF00538; Linker histone; I. PRINTS; PR00624; HISTONEH5. PRODOM; PD000373; Linkerhist N; 1. SMART; SM00526; H15; 1. SMART; SM00526; H15; 1. SMART; SM00526; H15; 1. Chromosomal protein; Nuclear protein; DNA-binding; Multigene family. SEQUENCE 210 AA; 21746 MW; 08C38P64894007E2 CRC64;	WISS-PROT entry is copyright. It is produced through a n the Swiss Institute of Bioinformatics and the EMB ropean Bioinformatics Institute. There are no restrity non-profit institutions as long as its content is ed and this statement is not removed. Usage by and es requires a license agreement (See http://www.isb-sid an email to license@isb-sib.ch).	SEQUENCE FROM N.A. TISSUE=Embryo; MEDLINE=S7040778; PubMed=3022245; MEDLINE=S7040778; PubMed=3022245; KnowLes J.A., Childs G.J.; KnowLes J.A., Childs G.J.; Comparison of the late H1 histone genes of the sea urchins Lytechinus pictus and Strongelocentrotus purpuratus."; Nucleic Acids Res. 14:8121-8133(1986). Nucleic Acids Res. 14:8121-8133(1986). THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES. SUBCELULLAR LOCATION: Nuclear. SUBCELULLAR LOCATION: Nuclear. SUBCELULLAR LOCATION: Nuclear.	RESULT 1 H1_LYTPI STANDARD; PRT; 210 AA. PRT 01-JAN-1988 (Rel. 06, Created) DT 01-JAN-1988 (Rel. 06, Last sequence update) DT 15-JUL-1999 (Rel. 38, Last annotation update) DE Late histone H1. OS Lytechinus pictus (Painted sea urchin). OC Eukaryota, Metazoa; Echinodermata; Eleutherozoa; Echinozoa; CC Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae; OC Lytechinus. OC Lytechinus. OC Lytechinus. OC Lytechinus. OX NCBI TaxID=7653;

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MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
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              <del>:</del>
                                                                                     Lubkowski J., Hennecke F., Plueckthun A., Wlodawer Filamentous phage infection: crystal structure of with its correceptor, the C-terminal domain of Tola. Structure 7:711-722(1999)
                                                                                                                                                                               "TolA central domain intera
EMBO J. 15:6408-6415(1996).
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Bscherichia coli.";
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Enterobacteriaceae; Eschei
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                                                                                                                                                                                                        Derouiche R
Lloubes R.;
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Levengood S.K., Beyer W.F. Jr., Webster R.E.;
"TolA: a membrane protein involved in colicin
extended helical region.";
Proc. Natl. Acad. Sci. U.S.A. 88:5939-5943(199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=K12;
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                                                                                                                                        MEDLINE=99332679; PubMed=10404600;
                                                                                                                                                                                                                                  INTERACTION WITH PORINS.
MEDLINE=97133271; PubMed=8978668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97061202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequences of the tolk and tolk genes and localization
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            BINDING TO THE BACTERIA. ALSO INVOLVED OF BACTERIOPHAGE DNA.
SUBUNIT: INTERACTS, VIA DOMAIN II, WITH
                                                 FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF GROUP; COLICINS (COLICINS A, E1, B2, B3, AND K). NECESSARY FOR THE COLICINS TO REACH THEIR RESPECTIVE TARGETS AFTER INITIAL
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EMBL; AE000177; AAC73833.1; --
EMBL; D90713; BAA35405.1; --
EMBL; JV0057; JV0057.
PDB; 1TOL; 20-MAY-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                    Eukaryota; Metazoa; Arthropoda; Hexapoda; Inso
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                  Drosophila hydei (Fruit fly).
                                                                                                                                                                              01-FEB-1995
16-OCT-2001
                                                                                                                                                                                                             Q08696;
                                                                                                                                                                                                                                DROHY
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CYTOPLASMIC (POTENTIAL).
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FUNCTION: POSSIBLE
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           225:1089-1095(1994)
                                                                             ., AND CHARACTERIZATION PubMed=7957199;
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                                                                                                                                                                                                                                                                                                                     46.0%;
 STRUCTURAL
                                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                     mst101(2).
                                                                                                                                                                                                                                                                                                           Score 98; DB
Pred. No. 0.00
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN II (ALPHA-HELICAL).

DOMAIN III (FUNCTIONAL).

10 X TANDEM REPEATS OF [ED]-K(1,2)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PERIPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                   8B2F52B4B97C655E CRC64
 ROLE
                                                                                                                                                                                                                      1391
                                                                                                                                                                                                                                                                                                                      DB 1;
0.0073;
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  THE
                                                                                                                                         Insecta; Pterygota;
  SPERM
                                                                                                                               Muscomorpha;
                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                               Length 421;
                                                                                                                                                                                                                                                                        294
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DESCRIPTION OF THE PROPERTY OF
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          smegmatis.";
Mol. Gen. Ger
-!- FUNCTION:
                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboratio between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no ware modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Last annotation update)
DNA-binding protein HU homolog (Histone-like protein) (Hlp)
HUP OR HLP.
                         InterPro; IPR000119; Bac_DNAbind.
Pfam; PF00216; Bac_DNA_binding; 1.
ProDom; PD000945; Bac_DNAbind; 1.
                                                                                                                 EMBL; AF068138; AAD13809.1; -. HSSP; P02346; 1HUU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=ATCC 700084 / mc(2)155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterineae; Mycobacteriaceae; Mycobacterium
NCBI_TaxID=1772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium smegmatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBgn0020733; Dhyd\mst101(2).
Sperm; Repeat; Multigene family; Polymorphism.
Sperm; Repeat; Multigene family; Polymorphism.
TANDEM REPEATS
DOMAIN
332 1268 [KR]-K-X-C-X-X-A-K-X-X-K-X-X-X-E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Upregulation of a histone-like protein in dormant Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99110209; PubMed=9894918;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gen. Genet. 260:475-479(1998).
FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF PROKARYOTIC DNA-BIDDING PROTEINS WHICH ARE CAPABLE OF WRAPPING DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
POLYMORPHISM: LENGTH POLYMORPHISMS EXIST BETWEEN DIFFERENT
STRAINS, MOST LIKELY CAUSED BY LENGTH VARIATIONS WITHIN TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: SPERMATIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S51364; S51364.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murugasu-Oei B., Dick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1391 AA;
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(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
Bac_DNAbind;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 90; DB;
; Pred. No. 0.13
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1B2A368F30F48878 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
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                                                                                                                                                                                                                                                                                                                                                                                          a collaboration
                                                                                                                                                                                                                                                                     for commercia.
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                                                        Best Local
Matches
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                                                                                Query Match
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PROSITE; P800045; HISTONE LIKE; 1.

DNA-binding; DNA condensation; Repeat.

DOMAIN 1 90 BACTERIAL HISTONE-LIKE DOMAIN.

DOMAIN 101 205 CASPS77P61F7EP09 CRC64;
                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a colla between the Swiss Institute of Bioinformatics and the EMBL outs the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for coentities requires a license agreement (See http://www.isb-sib.ch/a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H18_STRPU
P15869;
                                                                                                                                                                            InterPro; 1PR005819; Histone H5.
InterPro; IPR005216; Linkerhist N.
InterPro; IPR003216; Linker histone; T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strongylocentrotus purpuratus (Purple sea urchin).
Bukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
Strongylocentrotus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1990 (Rel. 14, Last seque 15-JUL-1999 (Rel. 38, Last annot Histone H1-beta, late embryonic
                                                                                                                                                                                                                                         PIR; A28100; A28100.
HSSP; P02259; 1HST.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Strongylocentrotus purpuratus.";
MO1. Cell. Biol. 8:1842-1844 (1988).
-I- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
                                                                                                                                        ProDom; PD000373; L1;
SMART; SM00526; H15;
                                                                                                                                                                   Pfam; PF00538; linker history PRINTS; PR00624; HISTONEH5.
                                                                                                                                                                                                                                                                     EMBL; M20314; AAA30052.1; -.
                                                                                                                                                                                                                                                                                                  or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the gene encoding the late histone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1990
01-APR-1990
                                                                                                                                                                                                                             InterPro; IPR005818; Histone_H1/H5.
                                                                                                                                                                                                                                                                                                                                                                                                                - I - SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lai Z.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=88246461; PubMed=2837660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Nuclear
 139
                                                        26; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
                                                                                                                                                                                                                                                                                                  g requires a license agreement (S
an email to license@isb-sib.ch).
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                                                                                                                                                       PD000373;
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SKKTTKKVKKPAAKKAKKPA-AKKAAK--KPAAKKPAAKKAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Childs
                                                                                                              211 AA;
                                                                                                                             protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 14, Created)
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                                                                                                                                                   Linkerhist_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G.; of the structure
                                                                                                              ; Nuclear protein; DNA-binding; Multigene family. 22169 MW; 9F214581334BBE7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.0%;
                                                                  42.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence update)
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T
                                                     Score 89.5; DB
Pred. No. 0.026;
3; Mismatches
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Pred. No. 0.
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and transcriptional patterns of subtype H1-beta of the sea urch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211
                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ζ
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                                                                                 DB 1,
                                                          10;
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                                                                                 Length 211,
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                                                        Indels
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                                                        Gaps
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DBH_MYC
P95109;
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                                                                                                                                                                                                                                                                           Submitted (DEC-1997) to the SWISS-PROT data bank.

-!- FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME ENVIRONMENTAL CONDITIONS (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
           SMART; SM00411; BHL; 1.
PROSITE; PS00045; HISTONE_LIKE; 1.
                                 InterPro; IPR000119; Bac_DNAbind.
InterPro; IPR005819; Histone H5.
Pfam; PF00216; Bac_DNA_binding; 1.
PRINTS; PR00624; HISTONEH5.
PRODOm; PD000945; Bac_DNAbind; 1.
                                                                                                                               EMBL; Z83018; CAB05427.1; -. EMBL; AB007127; AAK47393.1; PIR; G70673; G70673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Feterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=H37Rv;
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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HUD OR HLD OR LBP21 OR RV2986C OR MT3064 OR H
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Infect. Immun. 59:3685-3693(1991).
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MEDLINE=91372983; PubMed=1894368;
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Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H.,
Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi
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PROSITE; PS00732; RIBOSOMAL_S16; FALSE_NEG
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ProDom; PD003791; Ribosomal_S
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MBL outstation -
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Gordon S.V., Biglmeier K., Gas S., Barry C.B. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh; Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Pleischmann R.D., Hickey E., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Fotonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Kolonay J.F., Nelson W.C., Umayam J., Khouri H., Gill J., Mikula Pelcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=M.tuberculosis; STRAIN=H37Rv; MEDLINE=98295987; PubMed=9634230; Cole S.T., Brosch R., Parkhill J., Ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION SPECIES=M.tuberculosis, and M.bovis; STRAIN=H37Rv, ATCC 201 / H37Ra, and BCG / Paris 1173 P2; MEDLINE=98445421; PubMed=9770536;
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SPECIES=M.tuberculosis, and M.bovis;
STRAIN=ATCC 201 / H37Ra, and BCG / Paris 1173
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                                                                                                                                                                                                                                                                                                                                                  extrapulmonary dissemination.";
Nature 412:190-194(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97188915; PubMed=9064359;
Menozzi F.D., Rouse J.H., Alavi M., Laude-Sharp M.,
Bischoff R., Brennan M.J., Locht C.;
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Menozzi F.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Identification of a heparin-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                      "The heparin-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Whole genome comparison of Mycobacterium tuberculosis clinical and
FUNCTION: REQUIRED FOR EXTRAPULMONARY DISSEMINATION. MEDIATES ADHERENCE TO EPITHELIAL CELLS BY BINDING TO SULFATED GLYCOCONUUGATES PRESENT AT THE SURFACE OF THESE CELLS; BINDS HEPARIN, DEXTRAN SULFATE, FUCOIDAN AND CHONDROITIN SULFATE. PROMOTES HEMAGGLUTINATION OF ERYTHROCYTES OF CERTAIN HOST SPECIES. INDUCES MYCOBACTERIAL AGGREGATION. SUBCELLULAR LOCATION: SURFACE ASSOCIATED. DOMAIN: HEPARIN BINDING SEEMS TO REQUIRE THE C-TERMINAL DOMAIN OF HBHA. PROGRESSIVE TRUNCATIONS FROM THE C-TERMINAL DOMAIN OF HBHA. PROGRESSIVE TRUNCATIONS FROM THE C-TERMINAL DOMAIN OF HBHA. PROGRESSIVE TRUNCATIONS FROM THE C-TERMINAL END DIMINISH THE AFFINITY FOR HEPARIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
CONFLICT
                                                                                                              "The Drosophila hydei gene Dhmst101(1) encodes a testis-specific, repetitive, axoneme-associated protein with differential abundance Y chromosomal deletion mutant flies.";
Dev. Biol. 162:414-425(1994).
-i- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL. IT IS
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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16-OCT-2001
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Cell adhesion
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EMBL; Z77162; CAB00936.1; -.
EMBL; AE006951; AAK44716.1; ALT_INIT
PIR; F70742; F70742.
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                                                                                                                                                                               Neesen J., Buenemann H.,
                                                                                                                                                                                                                                                          Ephydroidea; Drosophilidae;
                                                                                                                                                                                                                                                                                                Drosophila hydei (Fruit fly)
                                                                                                                                                                                                                                                                                                             MST101(1)
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                                      +
                                                                                                                                                                                           MEDLINE=94200512; PubMed=8150205;
                                                                                                                                                                                                                   SEQUENCE FROM N.A.,
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                                                                                    ASSOCIATED WITH AXONEMAL STRUCTURES SUBCELLULAR LOCATION: Cytoplasmic ()
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                                      POLYMORPHISM:
                                                             TISSUE SPECIFICITY: TESTIS. SPERMATID BUNDLES.
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                                                  DOMAIN: THE PREDOMINANT STRUCTURE IS
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SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                TaxID=7224;
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198 AA;
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120 R
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Pred. No.
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R -> P (IN REF. 1).
; 513760F6F1EB6042 CRC64;
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                                    BETWEEN STRAINS.
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RESULT 11
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This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                        MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufinagle w.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Waadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001
16-OCT-2001
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01-OCT-1996
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Sperm; Repeat; Multigene family.
DOMAIN 58 337 19 X 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as modified and this statement is not removed. U entities requires a license agreement (See htt
                                                                                                                                                                opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                Submitted (AUG-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                     Dennis J.J., Lafontaine E.R., Sokol I "Identification and characterization Pseudomonas aeruginosa.",
J. Bacteriol. 178:7059-7068 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOLA
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                                                                                                                                                                                                                                                                                                         STRAIN-ATCC
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TOLA OR PA0971
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                                                                                                                                                                                             "Complete genome sequence of Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                          REVISIONS TO N-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97113525; PubMed=8955385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CBI_TaxID=287;
                                                                                                                          SUBCELLULAR LOCATION:
                                                                                                                                                     FUNCTION: INVOLVED IN
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K-K-K-C-X-E-X-A-{KQ}-K-X-X-E-X-A-X.
; 24C65D2510387E2A CRC64;
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Matches 24
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QSXBI8; Q9S5U5;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Interes are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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EMBL; AE004530; AAG04360.1;
PIR; E83525; E83525.
                     InterPro; IPR000119; Bac_DNAbind.
InterPro; IPR005819; Histone H5.
Pfam; PF00216; Bac_DNA binding; 1.
PRINTS; PR00624; HISTONEH5.
ProDom; PD000945; Bac_DNAbind; 1.
SMART; SM00411; BHL; 1.
                                                                                                                                                                            EMBL; Y18421; CAB46493.1; -.
EMBL; AB013441; BAA78330.1; -.
HSSP; P02346; 1HUU.
                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification of a novel protein generating bacterial from Mycobacterium.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prabhakar S., Tyagi J.S., Prasad H.K.; "HLPMt-A target for differentiation of M.tuberculosis and M.bovis."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterineae, Mycobacteriaceae, Mycobacterium.
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TIGRFAMs; TIGR01352; tonB_Cterm; 1.
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HISTONE_LIKE; 1
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37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
U homolog (Histone-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matsuo T., Mineda T., Yamada protein generating bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 0.006; Mismatches
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                                                                                                                                                                                                                                                                                                  noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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OF WRAPPING
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SEPPER

Histone H1, gonadal.

Parechinus angulosus (Angulate sea urchin).

Eukaryota; Metazoa; Echinodermata; Eleutherozoa;

Echinozoa;

H1 PARAN P02256; 21-JUL-1986 21-JUL-1986 15-JUL-1999

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RESULT 13
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RESULT 14
H1_PARAN
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Best Local Similarity .
Matches 22; Conserva
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Q8NNX3;
28-FEB-2003
28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DOMAIN
1 90 BETERIAL HISTONE-LIKE DOMAIN.
DOMAIN
1 205 DEGENERATE REPEATS REGION.
CONFLICT 199 199 A -> T (IN REF. 2).
SEQUENCE 205 AA; 21262 MW; 19FCE67885DFE6A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AP005280; BAB99447.1; -. HAMAP; MF_00385; -; 1. InterPro; IPR000307; Ribosomal
                                                                                                                                                                                                                                                                                                                                  TIGRPAMM, TIGRO0002; S16; 1.

PROSITE; PS00732; RIBOSOMAL S16; FALSE NEG
RIBOSOMAL PROTECTION: Complete Proteome.

SEQUENCE 165 AA; 17837 MW; 61DD81961BC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genomic sequence of Corynebacterium glutamicum ATCC 130 Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-I- SIMILARITY: BELONGS TO THE S16P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriae; Corynebacteriae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; Pr00886; Ribosomal_S16; 1.
ProDom; PD003791; Ribosomal_S16; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corynebacterium glutamicum (Brevibacterium flavum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPSP OR CGL2054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nakagawa S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1718;
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                                                                                                                                               KAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEA
                                                                                                                   EAITEKKKAREDKEAKEAA--EKAAAEKAAAAES
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                                                                                                                                                                                                                          Score 82; DB 1
Pred. No. 0.11;
4; Mismatches
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Pred. No. 0.061;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                        61DD81961BC30846 CRC64;
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                                                                                                                                                                                                                                                                                 DB 1;
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                                                                                                                                                                                                                                                                              Length 165;
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RESULT 15
H1E_CHIPA
ID H1E_CHIPA
AC P40262;
DT 01-FEB-1995
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Best Local
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                                                                                              SEQUENCE FROM N.A.

Schulze E., Wisniewski J.R., Nagel S., Gavenis K., Grossbach
Submitted (XXX-1994) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION
NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
                                                                                                                                                                                                                                                                                 Chironomus pallidivittatus (Midge).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Chironomoidea;
Chironomidae; Chironomus.
                                                                                                                                                                                                                                                                                                                                                                                                Histone H1E.
                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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ProDom; PD000373; Linkerhist_N; 1.
SMART; SM00526; H15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A91090; HSURIP.
HSSP; P02259; 1HST.
HSTP: P02259; 1HST.
InterPro; IPR005818; Histone H5.
InterPro; IPR005819; Histone H5.
InterPro; IPR003216; Linkerhīst N.
Pfam; PF00538; linker histone; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The primary structure of histone H1 from sperm of the sea urchin Parechinus angulosus. 2. Sequence of the C-terminal CNBr peptide at the entire primary structure.";
Eur. J. Biochem. 104:567-578(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=80156832; PubMed=7363905; Strickland W.N., Strickland M., B Wittmann-Liebold B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The primary structure of histone H1 from sperm of the sea urchin Parechinus angulosus. 1. Chemical and enzymatic fragmentation of the protein and the sequence of amino acids in the four N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=80156831; PubMed=6767609;
Strickland W.N., Strickland M., de Groot P.C.,
Wittmann-Liebold B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae; Parechinus.
  This
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                                                                                                                                                                                                                                                              NCBI_TaxID=7151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chromosomal
                                                SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Nuclear. TISSUE SPECIFICITY: SPERM.
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SWISS-PROT entry is copyright.
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Matches 26
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                                                                                                                                                                      SEQUENCE
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ProDom; PD000373; Linkerhi
SMART; SM00526; H15; 1.
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InterPro; IPR003216; Linkerhist N.
Pfam; PF00538; linker_histone; 1.
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the European
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l Similarity 41.3%;
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pean Bioinformatics Institute. There are no re
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IPR005819;
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235 AA; 2
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Search completed: January 21, 2004, 09:00:58 Job time: 8.13636 secs

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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1: sp_archea:*
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4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_vertebrate:
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213
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Domann E., Domann E., Entian K.-D., Fsihi H., Entian K.-D., Goebel W.,
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           Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A., Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T., Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P., Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussur Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P., Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jack
                                                                                                                                                                                                                                                                                                        Hypothetical protein lmo1941. LMO1941.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=06:H1 / CFT
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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Tola or C0818.
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                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 Listeria monocytogenes.
Listeria monocytogenes,
-- virmicutes; Bacillales;
                                                                                                                                             STRAIN=EGD-e / Serovar 1/2a;
MEDLINE=21537279; PubMed=11679669;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.035;
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Q92A67; Q92A67; 01-DEC-2001 01-DEC-2001 01-MAR-2003

(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.

19, 19, 23,

Created)

Last sequence update)
Last annotation update)

PRELIMINARY;

243

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RESULT 5
Q92A67
ID Q92A
AC Q92A
DT 01-D
DT 01-D
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Q9AJX2
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InterPro; IPR002402; LysM.
Pfam; PF01476; LysM; 1.
SMART; SM00257; LysM; 1.
SHypothetical protein; Complete p:
SEQUENCE 239 AA; 25836 MW; 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9AJX2; PRELIMINARY;
Q9AJX2;
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-MAR-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Pu Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A., Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P., "Comparative genomics of Listeria species."; Science 294:849-852 (2001).
                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                        Bentley S.D., Chatter K.F., Cerdeno-Tarraga A.-M., Challis G.L., Bentley S.D., Chatter K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quali M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.
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SCO1805 OR SCI33.04.
                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                  "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomycineae; Streptomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                      Nature
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AL939110; CAC28545.1; -.
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244 AA;
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                                                                                                                       SOKVAAIBAKKEAAAKKATAKKATAEKKAAAEKAAAKRAAKE 119
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nilarity 56.2%;
Conservative
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17,
23,
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                                                                                                                                                                           Score 91; DB:
Pred. No. 0.1;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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Pred. No. 0.045;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last annotation update)
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72E59D576E0D7832 CRC64;
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                                                                                                                                                                                                      DB 16; Length 244;
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Parkhill J.,
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RESULT
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OOL 100
OOL 10
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Matches 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Axoneme-associated protein MST101(3).
MST101(3) OR DHMST101
                                                                                                                                                                                                                                                                                          Neesen J., Heinlein U.A.O., Buenemann H.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002482; LysM.
Pfam; PF01476; LysM; 1.
SMART; SM00257; LysM; 1.
Hypothetical protein; Complete proteome.
Hypothetical protein; Complete proteome.
                                                                                             FlyBase; rby...
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical LIN2055.
     SEQUENCE
                                                                                                                                                            -!- TISSUE SPECIFICITY: TESTIS
-!- DOMAIN: THE PREDOMINANT STR
EMBL; U85627; AAB51369.1; -
                                                                                                                                                                                               SIMILARITY).
-i- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: TESTIS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila hydei (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 294:849-852(2001).
EMBL; AL596170; CAC97285.1;
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PubMed=11679669;
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                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKKYA-KKAKAEKAKKAYKAAEAKKA-----
                                                                                                                                   FBgn0020732; Dhyd\mst101(3).
     275
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64 255
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                                                                                                          family.
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                                                                                                                                                                                    STRUCTURE
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.13
3; Mismatches
                                                    13 X 16 AA APPROXIMATE TANDEM REPEATS X-[KQ]]-K-C-[AE]-E-X-A-[X]-K-X-X-X-X-
[AE]-X.
76BAA7B2A2DF732C CRC64;
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                                                                                                                                                                                       ALPHA-HELICAL
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RESULT 8
Q9A5J6
ID Q9A5
AC Q9A5

Q9A5J6;

PRELIMINARY;

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RESULT 7
Q9WWYXI
DD Q9WW
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Best Local Similarity
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"The Pseudomonas putida peptidoglycan-associated outer membrane lipoprotein (PAL) is involved in maintenance of the integrity of cell envelope.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999
01-MAR-2003
                                                                                                                                                                                                                                                                     TIGRFAMB; TIGR01352; tonB_Cterm; SEQUENCE 372 AA; 40133 MW; 8
                                                                                                                                                                                                                                                                                                         PRINTS; PR00624; HISTONEH5.
                                                                                                                                                                                                                                                                                                                                                                                         Rodriguez-Herva J.J., Ramos J.;
"Characterization of an OprL null mutant
J. Bacteriol. 178:5836-5840(1996).
EMBL; X74218; CAB50780.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rodriguez-Herva J.J.;
Submitted (JUL-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas putida.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9WWX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96422022; PubMed=8824639;
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Submitted (JUN-1995)
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                                                                                                                                                                                                                                                                                                                                           InterPro; IPR005819; Histone_H5.
InterPro; IPR006260; TonB_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteriol. 178:1699-1706(1996)
  181
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  AEEAKKKA 188
                                                                                        AEDAAKAAEAAKAAEAKKAAEAKKADEAKKAAEKQQADIAKKKAEDEAKKKAEEEAKKAA 180
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23,
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                                                                                                                                                                               Score 88.5; D
Pred. No. 0.27
8; Mismatches
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Last sequence update)
Last annotation updat
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Pred. No. 0.
                                                                                                                                                                                                                                                                          87F49785ECC3C0BC CRC64;
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Best Local S
Matches 27
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Pfam; PF01751; Toprim; 1.
Pfam; PF01396; zf-C4 Topoisom; 1.
PRINTS; PR00417; PRTPISMRASEI.
SMART; SM00437; TOP1Ac; 1.
SMART; SM00435; TOP1Bc; 1.
SMART; SM004393; TOPRIM; 1.
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01-JUN-2001 (TrEMBL
01-MAR-2003 (TrEMBL
DNA topoisomerase (
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Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.,

"Complete genome sequence of Caulobacter crescentus.",

"Complete genome sequence of Caulobacter crescentus.",

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

-1- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE

CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER (BY
           01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2003 (TrEMBLrel. 23, 27cbable histone H1 protein. RSC2793 OR RS00453.
                                                                                                                                                                                                                                                                                                                                                     TIGRPAMS; TIGR01051; topA bact; 1.
PROSITE; PS00396; TOPDISOMERASE I PROK; 1.
DNA-binding; Isomerase; Topoisomerase; Com;
SEQUENCE 899 AA; 97723 MW; 1485DC4EDA01
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                                                                                                   Q8XVN7;
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InterPro; IPR003602; DNAtopI DNA_bind.
InterPro; IPR003603; DNA_topI bact.
InterPro; IPR00380; DNA_tpisomrase.
InterPro; IPR006171; Toprim_dom.
InterPro; IPR006154; Toprim_sub.
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CATALYTIC ACTIVITY: ATP-INDEPENDENT BREAKAGE OF SINGLE-STRANDED DNA, FOLLOWED BY PASSAGE AND REJOINING.

DNA, FOLLOWED BY PASSAGE AND REJOINING.

MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA BACKBONB BOND, IT SIMULTANEOUSLY FORMS A PROTEIN JUNA LINK, IN WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS AT ONE END OF THE ENZYME-SEVERED DNA STRAND (BY SIMILARITY).

SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FAMILY
                                                                                                                                                                                                               836
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P06612; IECL.
CC2451; -.
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                                                                                                                                                                                                                                                                                                 Similarity
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FCC 19089 /
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                                                                                                                                                                                                                                            АККУАККАКАЕКАК-КАУКААЕАККААКУЕКАААЕКАААКЕААУЕА 45
solanacearum (Pseudomonas solanacearum)
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
merase (EC 5.99.1.2).
                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                   Conservative
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Last sequence tast annoted
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Pred. No. 0.71
5; Mismatches
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1485DC4EDA0DA6FA CRC64;
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annotation update)
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0.71;
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RESULT 10
Q8PI40
ID Q8PI4
AC Q8PI4
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Natura A.C., Alliana J.P., Tamura R.E., Teixeira B.C., Tezza R.I.D., Noset Specificities.";
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Query Match
Best Local Similarity
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01-OCT-2002
01-MAR-2003
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BMBL, AL646071; CAD16500.1; -.
InterPro; IPR005819; Histone_H5.
PRINTS; PR00624; HISTONEH5.
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Arlat M., Billault A., Brottier P., Camus J.C., Cattolicy
Chandler M., Choisen N., Claudel-Renard C., Cunnac S., Dy
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Scl
Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FF
STRAIN=306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaprot
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                                                                                                                                                                Nature 417:459-463(2002).
EMBL; AE011948; AAM37903.1; -.
InterPro; IPR005819; Histone_H5
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                                                                                                                                            PRINTS; PR00624; HISTONEH5
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                                                                                    proteome.
155 AA;
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PubMed=12024217;
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52.0%;
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Pred. No. 0.24
4; Mismatches
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                                                                                                                                                                                                                                             "Identification of Candida albicans protein domains with transcriptional activating properties in Saccharomyces cerevisiae."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

NON TER 1 1 1 SEGÜTENCE 1 1
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Eukaryota; Fungi; Ascomycota;
Saccharomycetales; mitosporic
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01-MAY-1999 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
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Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=152794;
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01-MAR-2003
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Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H.,
Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi
Usuda Y., Sugimoto S.;
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23; Conser
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llarity 48.9%;
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                                                                                                                                                             "Papageorgiou F., Soteriadou K.;
"Identification of a Leishmania infantum gene
H1-like nuclear protein.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tzortzakis N., Papageorgiou F.T., Tzinia A.K., Soteriadou K.P.; "Identification and characterization of a novel Leishmania gene encoding for a putative histone H1- like transcription factor.", Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ237814; CAD21431.1; -.
EMBL; AJ237814; CAD21431.1; -.
EMBL; EMBL/GenBank/DDBJ databases.
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Leishmania infantum.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
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                                                                                                                   Nuclear protein. SEQUENCE 111 A
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l Similarity 55.0%;
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3; Mismatches
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Pred. No. 0.19
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Page 6
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Search completed: January 21, 2004, 09:00:26 Job time: 21.1169 secs
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                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN-BPW28;

MEDLINE-95319329; PubMed=7596289;

MEDLINE-95319329; PubMed=7596289;

Scarlato V., Arico B., Goyard S., Ricci S., Manetti R., Prugnola A., Manetti R., Polverino-De-Laureto P., Ullmann A., Rappuoli R.;

"A novel chromatin-forming histone H1 homologue is encoded by a dispensable and growth-regulated gene in Bordetella pertussis.";

Mol. Microbiol. 15:871-881(1995).

EMBL; L37438; AAB59120.1; -.

EMBL; L37438; AAB59120.1; -.

SEQUENCE 182 AA; 18252 MW; 9A17A397B12B0421 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
NCBI_TaxID=520;
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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being part and is derived by analysis of the total score distribution.

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AAR28871	AAR06446	AAY82571	AAY82574	AAY82576	AAY82575	AAY82573	AAY82577	AAY82572	ID		
High affinity macr	Recombinant copoly	Copolymer molecula		Copolymer molecula	Description						

Human polypeptide	ABP62855	23	221	35.4	75.5	5
Protein differenti	ABU07443	24	220	35.4	75.5	4
Human ribosomal L1	AAU76972	23	220	35.4	75.5	ü
Human secreted pro	AAG00759	21	218	35.4	75.5	2
Human secreted pro	AAG00755	21	218	35.4	75.5	Ξ
-	ABP62982	23	216	35.4	75.5	ö
Human ovarian anti	ABP41465	23	201	•	75.5	9
	ABP00299	23	111	•	75.5	8
phila	ABB58855	22	157	•	76	37
a	AAY57358	21	226	36.2	77	8
Human histone H1 i	AAY34060	20	226	36.2	77	5
Ħ	AAY57331	21	222	36.2	77	4
H	AAY34033	20	222	36.2	77	ພ
H1	AAW29476	18	222	36.2	77	ະ
one H1	AAY57366	21	158	36.2	77	μ
Histone H1 isoform	AAY34068	20	158	36.2	77	ŏ
0	AAY57364	21	116	36.2	77	9
Histone H1 isoform	AAY34066	20	116	36.2	77	8
0	AAY57365	21	103	36.2	77	27
	AAY34067	20	103	36.2	77	
Drosophila melanog	ABB60086	22	2151	36.4	77.5	25
Drosophila melanog	ABB63276	22	299	36.4	77.5	24
Tumour neoangiogen	ABG71044	23	80	38.0	81	3
C glutamicum prote	AAG91997	22	165	38.5	82	22
C albicans apoptos	AAG70868	22	427	39.9	85	2
Mycobacterium bovi	AAB20575	21	205	40.1	85.5	6
Pseudomonas aerugi	ABJ18771	24	347	40.4	96	9
_	AAW44936	19	198	40.4	96	8
•	AAW43082	19	198	40.4	86	7
Mycobacterial hepa	AAW44934	19	39	0	86	9
<	ABG28693	22	334			5
M. tuberculosis hi	AAY57353	21	214	2		4
M. tuberculosis hi	v	20	\vdash	N	ø	ü
Amino acid sequenc	AAY14928	20	223	ν.	91	2
Ç)	σ	1	S	44.1	9	F
Listeria monocytog	ABB49123	23	239	44.4	94.5	0

ALIGNMENTS

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RESULT 1
AAY82572
ID AAY8
AC AAY8
AC AAY8
AC AAY8
AC COPC
XX COPC
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KW Glat
KW oste
KW anti
KW anti
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KW Hasl
KW Hasl
KW Demy
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NO:2.

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyronimetic; haemostatic; antipporiatic; dermacological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; antianaemic; condition; multiple sclerosis; rheumatoid arthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; ohronic immune thrombocytopaenia gurpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; Hashimoto's disease; idiopathic myxoedema; myasthenia pemphigus vulgaris; systemic lupus erythematosus.

Unidentified.

WO200018794-A1

24-SEP-1999; 06-APR-2000 99WO-US22402.

25-SEP-1998; 98US-0101693.

(YEDA) YEDA RES & DEV CO LTD

(TEVA-) TEVA PHARM USA INC

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CC AAY92571 to AAY82577 represent specifically claimed copolymer molecular CC weight TV-marker polypeptides from the present invention. The present CC invention describes polypeptides (I) for determining the molecular cCC weight of a copolymer (CP), which has an identified molecular weight CC and an amino acid composition corresponding to the copolymer. The CC polypeptides of the invention are used as molecular weight markers for CC glatiramer acetate related terrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune CC diseases which may be treated include either cell-mediated or antibody-mediated diseases such diseases include arthritic conditions, cC demyelinating diseases such diseases include arthritic, autoimmune CC sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic canaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune CC uveoretinitis, Crohn's disease, chronic immune thrombocytopaenia CC disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic GC disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic GC disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic GC include host-versus-graft disease, graft-versus-host disease, and CC include molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local
                                                                                                                                                                                                                                         glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; from one disease; chronic immune thrombocytopaenia purpura; colitis; crohn's disease; chronic immune thrombocytopaenia purpura; colitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:7.
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WO200018794-A1
                                                                                                                                       pemphigus vulgaris; systemic
                                                                                                                                                                                                               diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              molecular weight markers.
                                                                                                                                                                             Hashimoto's disease; idiopathic myxoedema; myasthenia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        molecular weight marker; TV-marker; immune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 213; DB 21;
Pred. No. 1.6e-16;
Pred. No. 0;
                                                                                                                                           lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₽
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06-APR-2000

glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antificammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis;

Copolymer; molecular weight marker; TV-marker; immune disease;

Copolymer molecular weight TV-marker amino acid sequence SEQ ID

NO: 3.

2

28-JUL-2000 (first entry

Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;

Hashimoto's disease; idiopathic myxoedema; myasthenia

erythematosus

gravis;

Unidentified

pemphigus vulgaris; systemic

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RESULT 3
AAY82573
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                                                                                                                                                                                                                                                                                                                       contributed by the present invention. The present convention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight cand an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for complete acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune could diseases which may be treated include either cell mediated or cantibody-mediated diseases. Such diseases in clude arthritic conditions, completinating diseases and inflammatory conditions, autoimmune cophoritis, autoimmune thyroiditis, autoimmune cophoritis, autoimmune thyroiditis, autoimmune cophoritis, contact sensitivity disease, diabetes mellitus, Graves disease, chillian-barre's syndrome, Hashimoto's disease, disease, diabetes mellitus, Graves conditions, contact sensitivity disease, diabetes mellitus, Graves conditis contact sensitivity disease, diabetes mellitus, Graves conditions, contact sensitivity disease, diabetes mellitus, Graves disease, diabetes mellitus, Graves conditions, contact sensitivity disease, diabetes mellitus, Graves conditions, contact sensitivity disease, diabetes mellitus, Graves disease, and conditions, contact sensitivity. The polypeptides of the invention have conditions and physical properties which are analogous to conditions and properties which are analogous to conditions.
                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                               glatiramer acetate molecules, molecular weight markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
AAY82573 standard; peptide; 56
                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 10; Page 14; 72pp; English.
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(TEVA-) TEVA PHARM USA
                                                                                                                          5
                                                                                                                                                                                                                      36;
                                                                                                                                                                     Similarity
                                                                                                                          AKKYAKAAKAE--KKEYAAAEAKKAEAAKAYKAEAAKAAKEAAYEA
                                                                                                                                                                                                                                                                                                                       109 AA;
                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0101693.
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                                                                                                                                                                                                                                             64.8%;
76.6%;
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                                                                                                                                                                                                                      Score 138; DB 21;
Pred. No. 5.9e-08;
0; Mismatches 7
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                                                                                                                                                                                                                                                                    Length 109;
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RRESULT 4
AAX/8252
ID AAX/8
ID AAX/8
XX AAX/8
AC AAX/8
XX AAX/8
XX COpc
XX COpc
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XW Ostet
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Best Local (
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                   antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis;
                                                          glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological;
                                                                                                                          Copolymer; molecular weight marker; TV-marker; immune disease;
                                                                                                                                                                 Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:5.
                                                                                                                                                                                                             28-JUL-2000
                                                                                                                                                                                                                                                      AAY82575
                                                                                                                                                                                                                                                                                           AAY82575 standard; peptide; 77 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             molecular weight markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weighte and physical properties which are analogous glatiramer acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systlupus erythematosus. Mediated-mediated diseases which can be treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-317499/27
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TEVA PHARM USA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKY-KAEAAKAAAKEAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 14; 72pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                             (first
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                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 134.5; DB 21;
Pred. No. 7.2e-08;
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purpura;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of immune diseases
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28-JUL-2000 AAY82576; AAY82576

(first entry)

standard;

peptide; 86

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RESULT 5
AAY82576
ID AAY8
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AC AAY8
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AC AAY8
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                  antibody mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune opphoritis, osteoarthritis, autoimmune enveoretinitis, Crohn's disease, chronic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-bost disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;
Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune disease
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                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                       molecular weight
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(TEVA-) TEVA
                                                                                                                                                                    61
                                                                                                                                                                                                   30
                                                                                                                                                                                                                                                          39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TV-marker
                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                    YKAEAAKAAAKEAAYEA
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                                                                                                                                                                                                                                   AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
                                                                                                                                                                                                                                                                                                                                                                        77
                                                                                                                                                                                                                                                                                                    Conservative
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PHARM USA INC.
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                                                                                                                                                                                                                                                                                                                                                                                                         markers.
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                                                                                                                                                                                                                                                                                                                     61.5%;
                                                                                                                                                                      77
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                                                                                                                                                                                                                                                                                                                     Score 131; DB 21;
Pred. No. 2.4e-07;
                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present
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                                                                                                                                                                                                                                                                                                                                          77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diseases
                                                                                                                                                                                                                                                                                                       Gaps
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Copolymer; molecular weight marker; TV-marker; immune

Copolymer molecular weight

TV-marker amino acid

sequence

SEQ

ij

NO: 6

disease;

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                                                                                                                                                                                                                                                                                cc weight Tv-marker polypeptides from the present invention. The present convention describes polypeptides (I) for determining the molecular cc weight of a copolymer (CP), which has an identified molecular weight CC and an amino acid composition corresponding to the copolymer. The CC glatiramer acetate related tetrapolymers. The polypeptides may also be CC glatiramer acetate related tetrapolymers. The polypeptides may also be CC glatiramer acetate and preventing immune diseases in a mammal. Autoimmune CC diseases which may be treated include either cell-mediated or creating diseases and inflammatory conditions, e.g. multiple computations, autoimmune opphoritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune opphoritis, autoimmune thyroiditis, autoimmune CC uncertinitis, Crohn's disease, chronic immune thromocytopaenia CC myxoedema, mysathenia gravis, psoriasis, pemphigus vulgaris, or systemic CC include host-versus-graft disease, graft-versus-host disease, and celisued reythematosus. Mediated-mediated diseases which can be treated CC include host-versus-graft disease, graft-versus-host disease, and celisued molecular weights and physical properties which are analogous to CC glatiramer acetate molecules, which makes them ideal for use as
                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glatiramer acetate; autoImmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiniflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antidiabetic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohr's disease; chronic immune thrombocytopaenia purpura; collitis; disease; chronic immune thrombocytopaenia purpura; collitis;
                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; Page 14; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;
Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY82571 to AAY82577 represent specifically claimed copolymer molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
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  YKAEAAKKAYKAEAAKAAAKEAAYEA
                                                                                                                AKKYAKK-----AKAEKA-----KKAYKAAEAKKAAKYE------
                                                                          AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
                                                                                                                                                                                                                                                                      weight markers.
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                                                                                                                                                      Conservative
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                                    KAAAEKAAAKEAAYEA 45
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                                                                                                                                                                      Score
Pred.
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                                                                                                                                                      Mismatches
                                                                                                                                                    126.5; DB 21;
No. 8.3e-07;
smatches 6;
86
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                                                                                                                                                      41;
                                                                                                                                                    Gaps
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Query Match
Best Local Similarity 71.3
Matches 32, Conservative

56.6%;

Score 120.5; DB 2 Pred. No. 2.8e-06;

DB 21;

66; 7;

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0,

Mismatches

Indels Length

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2

Sequence

66

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RESULT 6
AAY82574
CC MAY82571 to AAY82577 represent specifically claimed copolymer molecular CC weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular CC invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The CC polypeptides of the invention are used as molecular weight markers for CC glatiramer acetate related testrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune CC diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, CC demyelinating diseases and inflammatory conditions, e.g. multiple CC sclements, autoimmune cophoritis, osteoarthritis, autoimmune haemolytic canaemia, autoimmune cophoritis, osteoarthritis, autoimmune haemolytic CC canaemia, autoimmune cophoritis, osteoarthritis, autoimmune cophoritis, contact sensitivity disease, diabetes mellitus, Graves CC purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves CC purpura, colitianes contact sensitivity diseases, didopathic condition myzoedema, myzathenia gravis, psoriasis, pemphigus vulgaris, or systemic condition heat versue-craft disease and diseases which can be treated conditions and disease and di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antianaemic; immunosuppressive; demyelinating disease; osteoarthritts; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                            include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous glatiramer acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copolymer; molecular weight marker; TV-marker; immune disease; glatiframer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glatiramer acetate and
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(TEVA-) TEVA PHARM USA INC.
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RESULT 7
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                                                        CC weight TV-marker polypeptides from the present invention. The present convertion describes polypeptides (1) for determining the molecular convertion describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight convertion acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for conjugation acid composition corresponding to the copolymer. The copolymeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune colleases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, colleases, theumatoid arthritis, obteoarthritis, autoimmune haemolytic canaemia, autoimmune cophoritis, autoimmune thryroiditis, autoimmune cophoritis, autoimmune thryroiditis, autoimmune cophoritis, autoimmune thryroiditis, autoimmune cophoritis, autoimmune thryroiditis, crothaves disease, chronic immune thropocytopaenia confisease, collitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic conficulate acide to the confist sand physical properties which can be treated confined molecular weights and physical properties which are analogous to defined molecular weights and physical properties which are analogous to conficular weight and properties which makes them ideal for use as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-317499/27
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RESULT 8
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Best Local
                                                                                                                                                                                      To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-19 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 US4691009, NREU B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences. A methionine residue occurs between the Protein A and rCOP-1 sequence, originating from the 5' linker sequence, in order that the COP-1 polypeptide may be cleaved from the fusion protein. rCOP-1: polypeptide may be cleaved from the fusion protein. rCOP-1: polypeptide may be cleaved from the fusion protein. rCOP-1: polypeptide may be cleaved from the fusion protein. rCOP-1: polypeptide may be cleaved from the fusion protein. rCOP-1: polypeptide may be cleaved from the fusion protein. rCOP-1: polypeptide may be cleaved from the fusion protein. rCOP-1: polypeptide may be cleaved from the fusion protein. rCOP-1: polypeptide may be cleaved from the fusion protein. rCOP-1: polypeptide may be cleaved from the fusion protein. rCOP-1: polypeptide may be cleaved from the fusion protein.
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                                                   See also
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17-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant copolymer 1; COP-1-19; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
03-JAN-1991
                                                                                  encephalomyelitis. They are used to prevent, arrest or control demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in
                                                                                                                                                                                                                                                                                                                                                                                                                                         Producing genes encoding random polymers of aminoacid(s) - for producing recombinant polypeptide(s) with biological and/or immunological activity
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                                                                                                                                      The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or
                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 12; 25pp; English
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                                                                                                                                                                       fusion protein.
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                               n amino acids.
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3d on 25-MAR-20
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                                   25-MAR-2003
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(first entry)
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89US-0312541.
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                                    correct PA field.)
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Pred. No. 3.4e-05,
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                                                                                                                                        arrest or control a
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Sequence

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DB 11;

Length 106;

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Best Local S
Matches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glycopeptide; mannose; mannosylated; glycosylated; mannose receptor; macrophages; monocytes; destroy; cytotoxicity; label; image; alter; macrophage processing of antigen; MHC restriction; inflammation; inflammatory diseases; macrophage secretory products; Crohn's disease; legionnaires disease; mononuclear phagocytes; HIV; Crohn's disease; legionnaires disease; mononuclear phagocytes; HIV;
                       Modified-site
                                                        Modified-site
                                                                                       Modified-site
                                                                                                                                                          Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organ transplantation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIDS; lysosomal storage diseases; Gaucher's disease; asthma; alveolar macrophages metastasis; systemic macrophages; deliver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High affinity macrophage mannose receptor ligand compound #9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
23-MAR-1993
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28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptides; prevent transplant rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (updated)
(first entry)
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"opt may have mannose, N-Ac-glucosamine."
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N-Ac-glucosamine."
                                                                                                                                                                               may have mannose,
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Pred. No. 0.00089;
4; Mismatches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agents; cancer; toxins.
                                                                                                                                                                                                                fucose,
                                                                                                                                                                                                                                                                                                                                                                                   fucose, glucose
           fucose, glucose or
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                                                                                                              fucose, glucose
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                                                                                                                                              glucose
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RESULT 10 ABB49123

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ABB49123;

ABB49123 standard; Protein;

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Listeria 05-FEB-2002

monocytogenes protein #1827

(first entry)

Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;

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                                                                                                                            This compound represents a glycopeptide effective in inhibiting the CC binding of labelled mannosylated BSA to mannose receptors. Mannose CC receptors are uniquely found on macrophages and not on monocytes. CC Glycopeptides such as this provide a mechanism to trayet macrophages. CC specifically, to image, label, destroy or otherwise alter their CC antigen processing function. In addition they can be conjugated to CC solid supports and used to purify mannose receptors from a variety CC of sources. They are useful in the treatment of inflammatory CC diseases driven by macrophage secretory products eg. Crohn's CC disease; infectious diseases in which macrophages harbour replicating CC infectious agents eg. Legionnaires disease; viral infections CC disease; in which macrophages harbour replicating CC involving mononuclear phagocytes eg. HIV and lysosomal storage CC involving mononuclear phagocytes eg. HIV and lysosomal storage CC diseases, in which macrophages are principally involved eg. CC daucher's disease; asthma mediated by alveolar macrophages, and in CC controlling metastasis, mediated by systemic macrophages, and cC can also be used to deliver antigenic peptides as conjugates to a CC macrophage to marchal an immune response; also self peptides to CC prevent tissue transplant rejection.
                                                            Best Loc
Matches
                                                                                         Query Match
                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 21; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New high affinity mannose receptor ligand cpds. - for diseases mediated by macrophage activity e.g. asthma, inflammatory diseases and infectious diseases, e.g. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1992;
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AAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA
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                                                            46.0%;
nilarity 63.4%;
Conservative
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                                                            Score 98; DB 13;
Pred. No. 0.00055;
L; Mismatches 14
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                                                                14;
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                                                                                            Length 46;
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                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                          monocytogenes and related organisms.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections, related polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chakraborty T, Domann E,
Perez-Diaz J, Baquero F,
Maduenio E, De Pablos B,
Rose M, Voss H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-APR-2000; 2000FR-0004629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-APR-2001; 2001WO-FR01118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-OCT-2001.
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   Recombinant
                                                                                                                                                  AAR06445 standard; protein; 154
                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; SEQ ID No 1828; 192pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dominguez-Bernal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Daniels J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Buchrieser C,
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                                                                                                                                                                                                                                      124
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                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B12; bacterial infection; disease.
                                                                                                                                                                                                                                   KAAAEKAEADKKKQEEDAVKAANAKKEQEAAEEKAAADKAAAEKAAAE 171
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                                                                                                                                                                                                                                                                                                                                                                    239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goebel W,
copolymer 1; COP-1-77;
                                copolymer 1-77, myelin basic protein analogue.
                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PASTEUR
                                                                 (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Frangeul L, Chetouani F,
                                                                                                                                                                                                                                                                                                                                                                    B
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                                                                                                                                                                                                                                                                                                                  44.4%;
56.2%;
                                                                                                                                                                                                                                                                                                  Score 94.5; DB 2
Pred. No. 0.0072;
7; Mismatches
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 myelin basic
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 protein; MBP
                                                                                                                                                                                                                                                                                                                                Length
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CC A methionine residue occurs between the Protein A and rCOP-1 genences, originating from the 5' linker sequence, in order that the COP-1 polypeptide may be cleaved from the fusion protein. CC rCOP-1-77 contains oligonucleotide duplexes incoding the following Cr rCOP-1-77 contains oligonucleotide duplexes 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
Mycobacterium vaccae protein; antigen; T cell activation; cytokine; dendritic cell maturation; infectious disease; immune disorder; canci respiratory system; mycobacterial infection; allergy; tuberculosis; leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis; dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunological activity; autoimmune encephalomyelitis;
multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Producing genes encoding random polymers of aminoacid(s) - producing recombinant polypeptide(s) with biological and/or immunological activity
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17-FEB-1989;
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                                                                                                                                         Amino acid sequence of M. vaccae antigen GV-45.
                                                                                                                                                                                         25-OCT-1999
                                                                                                                                                                                                                                                                                  AAY14928 standard; protein; 223
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AAQ05665.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     on 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 AA;
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89US-0312541.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 94;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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PX SX FX BX BX AX B
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                                                                                                                                                                                                                                    RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention provides heat-killed Mycobacterium vaccae, or recombinant CC M. vaccae proteins. The M. vaccae proteins may be employed to activate T cells and natural killer cells, to stimulate the production of CC cytckines, to enhance the expression of co-stimulatory molecules on CC dendritic cells and monocytes, and to enhance dendritic cell maturation and function. The proteins can be expressed by standard recombinant CC methodology. Pharmaceutical compositions comprising the proteins or nucleic acid sequences encoding the proteins can be used for the CC treatment, prevention, and detection of disorders including infectious CC diseases, immune disorders and cancer. In particular, the compounds and CC methods are used for treatment of diseases of the respiratory system, compensation as mycobacterial infections, asthma, allergies, tuberculosis, CC leprosy, sarcoidosis and lung cancers, and disorders of the skin such as psoriasis, atopic dermatitis, eczema, allergic contact dermatitis, allegations areata, and skin cancers such as basal carcinoma, squamous cell
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 28
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23-DEC-1997;
23-DEC-1997;
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11-JUN-1998;
17-SEP-1998;
                           Mycobacterium
                                                    Ulcerative colitis; histone; H1-like antigen; porin antigen; Bacteroides antigen; inflammatory bowel disease; IBD; pANCA; perinuclear anti-neutrophil cytoplasmic antibody.
                                                                                                                M. tuberculosis histone H1-like antigen.
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 239; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enhancing immune response to an antigen
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                                                                                                                                                                                                        AAY34055 standard; protein; 214 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 and melanoma.
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98US-0095855.
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97US-0997080.
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Pred. No.
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WO9945955-A1.

Cohavy O,

Braun J;

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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 25
                                                                                                                                                                                                                         Ulcerative colitis; inflammatory bowel disease; porin antigen; MAb; panCA; perinuclear anti-neutrophil cytoplasmic antibody; 214 protein; histone H1; isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of histone H1, porin or Bacteroides antigens as targets for diagnosis, prevention and treatment of ulcerative colitis {\color{black} \cdot}
                                                                                                                                                                                                Mycobacterium
                                                                                                                                                                                                                                                                                          M. tuberculosis histone H1-like protein,
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                                                          12-APR-1996;
11-APR-1997;
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                            (REGC ) UNIV CALIFORNIA
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25; Conservat
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nilarity 55.6%;
Conservative
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97US-0837058.
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Diagnosing ulcerative colitis or susceptibility, by detecting complex formation between microbial porin antigen and perinuclear anti-neutrophil cytoplasmic autoantibodies -

WPI; 2000-255695/22

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques
                                                                                                                                                                                                                                                                                                                                 31-MAR-2000;
23-AUG-2000;
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                                                                                                              Claim 20; SEQ ID No 59052; 103pp; English.
                                                                                                                                               New isolated polymucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                        WPI; 2001-639362/73
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2000US-0649167.
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                                                                                                                                                                                                                      CC (II) (II) is useful for generating antibodies against it, detecting or CC (III) (III) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polymucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity CC and to produce other types of data and products dependent on DNA and CC diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO
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214 ARKKAATETAEKAKAQADKKAAAEKAAADKKAAAEKAATDKKAAEKA 260
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27; Conserv
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213
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 2 US-09-816-989A-7 ; Sequence 7, Application US/09816989A

40	. 44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
69.0	69.5	•	70	70	70	70	70	70.5	70.5	70.5	71	71	71	71	72.5	73	74	74	74	74.5	75.5	75.5	75.5	77	77	77	77	77	77.5
32.0	32.6	32.6						•					•	33.3	34.0	34.3	34.7	34.7	34.7	35.0	35.4	35.4	35.4	36.2	36.2	36.2	36.2	36.2	36.4
1367	1130	578	1156	744	641	347	55	619	555	548	539	228	218	130	372	234	942	356	352	1002	265	220	201	226	222	158	116	103	227
10	, 12	12	9	11	ø	15	15	11	15	21	12	15	15	15	1	15	15	H	11	12	9	φ	12	15	15	15	15	15	15
02-10-130-701-13000	US-10-369-493-6751	US-10-032-585-7390	5-2	US-09-769-787-184	US-09-765-272-160	0-156-7	US-10-229-567-41	-09-882-774-1	US-10-128-714-8127	-10-128-	170	-10-156-761-	0-229	US-10-262-209-2	-69-	-10	US-10-156-761-12155	US-09-820-843A-27	US-09-820-843A-23	US-10-369-493-1378	59	US-09-923-304-2	US-10-264-049-2597	ည်	-10-229-567-	US-10-229-567-40	-10-229	US-10-229-567-39	US-10-156-761-10923
podromo 10000 5	sequence 6/51, Ap	7390,	13187,	e 184, A	160, 2	e 1165	41		Sequence 8127, Ap	e 3127,			Sequence 4, Appli	2					Sequence 23, Appl	Sequence 1378, Ap		-	Sequence 2597, Ap	e w	Sequence 3, Appli	_	<u>u</u>		e 1

ALIGNMENTS

US-09-816-989A-2

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                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Péptide US-09-816-989A-2
                                                                                                                                                                                                                                                                                                      APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT PILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: POT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
                                                                                    Query Match
Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09816989A Patent No. US20020115103A1
                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                      LENGTH: 45
1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
                         1 AKKYAKKAKAEKAKKAYKAAEKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                               100.0%;
|larity 100.0%;
|Conservative 0
                                                                                        0
                                                                                                         Score 213; DB 10;
Pred. No. 1.4e-16;
                                                                                        Mismatches
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                                                                                        Indels
                                                                                                                                Length 45;
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Best Local S
Matches 39
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Matches
                                  Sequence 5, Application US/09816989A Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.1 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09816989A Patent No. US20020115103A1
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                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide -09-816-989A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/616,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: FCT/US99/22402
PRIOR FILING DATE: 1998-09-24
PRIOR FILING DATE: 1999-09-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
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TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-FCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide -09-816-989A-7
APPLICANT: Gad,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                              LENGTH: 56
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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36; Conservative
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                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                     AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKY-KAEAAKAAAKEAAYEA 56
                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.8%;
76.6%;
                                                                                                                                                                                                                                               68.4%;
                                                                                                                                                                                                                               Score 134.5;
Pred. No. 5.66
0; Mismatches
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Pred. No. 4.8e-08;
0; Mismatches 7
                                                                                                                                                                                                                       DB 10;
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; APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR PILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOPTWARE: PatentIn version 3.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR TITLE OF INVENTION: AND FOR THERAPEUTIC USE FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR PILING DATE: 1998-09-26
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
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US-09-816-989A-6
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TYPB: PRT
TYPB: PRT
FRATURE:
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-5
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                                                                                                                                                                                                                                     US-09-816-989A-6
                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.1 SEQ ID NO 6
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APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
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Best Local Similarity
                                                                                                                                                           Matches
                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09816989A Patent No. US20020115103A1
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                                                                                                                                                                                                                                                                                           LENGTH: 86
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
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61
                                      30
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                                                                                                                    1 AKKYAKK-----AKAEKA-----KKAYKAAEAKKAAKYE--
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                                         -----KAAAEKAAAKEAAYEA 45
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                                                                             AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
                                                                                                                                                         Conservative
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                                                                                                                                                                              59.4%;
45.3%;
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Pred. No. 1.9e-07
                                                                                                                                                                              Score 126.5; DB 1
Pred. No. 6.5e-07;
                                                                                                                                                           Mismatches
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US-10-205-979-52
; Sequence 52, Application US/10205979
; Publication No. US20030147861A1
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                                                                          RESULT 8
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US-09-816-989A-4
                                                                                                                                                                                                                                                                                                                              US-09-816-989A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lib, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER: OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gad, Alexander APPLICANT: Lis, Doris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gad, Alexander APPLICANT: Lis, Doris
                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity 32; Conserv
                                                                                                                                                                                     1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 АККҮАККАКАЕКАККАҮКААЕАККААКҮЕКАААЕКАААКЕААҮЕА 45
                                                                                                                                                                                                                                                         Similarity
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larity 71.1%;
Conservative
                                                                                                                                                                                                                                                         50.7%;
                                                                                                                                                                                                                                 Score 108; DB 10;
Pred. No. 2.5e-05;
1; Mismatches 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 120.5; DB 10; Length 66; Pred. No. 2.2e-06; 0; Mismatches 6; Indels 7
                                                                                                                                                                                                                                                                              Length 35;
                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USE AS
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                                                                                                                                                                                                                                 Gaps
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RESULT 7

10-051-643-201

; Sequence 201, Application US/10051643

~ h11cation No. US20020197265A1
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; ORGANISM: Mycobacterium vaccae
US-10-205-979-52
                                                                                                                                                                             US-10-229-567-27
                                                                                                                                                                                                    RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-051-643-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 201
LENGTH: 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 52
LENGTH: 223
                                                                                                                   Sequence 27, Application US/10229567 Publication No. US20030092080A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/051,643
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US09/156,181
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: US 08/996,624
PRIOR FILING DATE: 1997-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 11000.1063U
CURRENT APPLICATION NUMBER: US/10/205,979
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/308,446
PRIOR FILING DATE: 2001-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Watson, James D. APPLICANT: Tan, Paul L. J. APPLICANT: Abernethy, Nevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: of Immunologically-Mediated Diseases of
TITLE OF INVENTION: System using Mycobacterium Vaccae
FILE REFERENCE: 11000.1008c2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Watson, James D. APPLICANT: Tan, Paul L. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Compounds and Methods for TITLE OF INVENTION: of Immune Responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 21
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Mycobacterium vaccae
                                                                                                                                                                                                                                                                                                                                                               ьосат
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                                     TITLE OF INVENTION: Diagnosis, Prevention and Treatment of Ulcerative Colitis, and Clinical Subtypes Thereof, Using
NUMBER OF SEQUENCES:
                                                                                                APPLICANT: Braun, Jonathan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137
                                                                                                                                                                                                                                                             137 AKKAATKAAPAKKATAAKKAAPAKKATAAKKAAPAKKAATKA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28;
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                                                                                                                                                                                                                                                                                                                                                               Similarity
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59.6%;
                                                                                                                                                                                                                                                                                                                                                             42.7%;
                                                                               Offer
                    Microbial UC pANCA antigens
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Pred. No. 0.013;
5; Mismatches
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Pred. No. 0.013;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12;
                                                                                                                                                                                                                                                                                                                                                                                DB 14; Length 223;
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CORRESPONDENCE ADDRESS

ADDRESSEE: Campbell & Flores LLP STREET: 4370 La Jolla Village Drive, Suite 700

STATE: California

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-127-032-120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
  Query Match
                                                                                                   SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 120
LENGTH: 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 120, Application US/10127032
Publication No. US20030113742A1
                                         ORGANISM: Pseudomonas aeruginosa
-10-127-032-120
                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/127,032
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/285,190
PRIOR FILING DATE: 2001-04-20
                                                                                                                                                                                                                                                                                                                  APPLICANT: Greenberg, Everett Peter
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION OF
TITLE OF INVENTION: BIOFILM FORMATION
FILE REPERENCE: UIZ-070CP
                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/344,142 PRIOR FILING DATE: 2001-10-24
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Whiteley,
                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/417,264
PILING DATE: <UNKNOWN>
APPLICATION NUMBER: US 09/041,889
PILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 AKKVAKKAPAKKATKAAKKAATKAPA---RKAATKAPAKKAATKA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/10/229,567
FILING DATE: 27-Aug-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 214 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                        Whiteley, Marvin
Bangera, M. Gita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                      Lory, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.0%;
55.6%;
  40.4%; Score 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 89.5; DB 15; Length 214; Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27:
  DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
Length 347;
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US-10-156-761-9889
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US-09-738-626-5751
                                                                                                           APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
SOFTWARE: Pate
SEQ ID NO 5751
LENGTH: 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9889
LENGTH: 376
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                     PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: JP 2001-272697 PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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Local Similarity 50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKKSAPAKKSAPGKTAAKKAAAKKTAPAKKSAAKKSAAKKTA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQKAAEAKKADEAKKAAEAKAAEQKKQADIAKKRAEDEAKKKAAEDA 171
                                                                                                                                                                                                                                                                                                         OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHIBA, TADAYOSHI
SAKAKI, YOSHIYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISHIKAWA, JUN
HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                   HAYASHI, MIKIRO
                                                                                                                                                                                                                                                                                                                                                                                                                        MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Application US/10156761
5. US20030119018A1
                                                                                                                                                                                                                                                                                       IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                        SEIKO
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Pred. No. 0.1;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 15; Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
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RESULT 15
US-09-820-843A-24
(S-09-820-843A-24
; Sequence 24, Application US/09820843A
; Publication No. US20030039963A1
; Publication No. US20030039963A1
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
; TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
; FILE REFERENCE: Q63915
; CURRENT APPLICATION NUMBER: US/09/820,843A
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 118
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US-10-156-761-12370
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US-09-820-843A-24
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
FILE REPERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UF 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: JF 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12370
LENGTH: 272
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Best Local Similarity 62.9%; Pred. No. 0.087;
Matches 22; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.0 SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 36.6%; Score 78; DB 15; Length 2.
Best Local Similarity 46.3%; Pred. No. 0.41;
Matches 19; Conservative 7; Mismatches 15; Indels
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APPLICANT:
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  ILENGTH: 309
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: polyhydroxyalkanoate synthesis protein PhaF
NAME/KEY: misc feature
OTHER INFORMATION: gi|9951352
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HORIKAWA, HIROSHI
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US-09-405-743A-7
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                                                                                                              SOFTWARE:
SEQ ID NO 7
LENGTH: 10
                                                                                                                                                                                                                                                        Sequence 7, Application US/09405743A
Patent No. 6514938
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 2
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Best Local Similarity
                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/405,743A CURRENT FILING DATE: 1999-09-24 NUMBER OF SEQ ID NOS: 7
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TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
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TYPE: PRT
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                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                               TYPE: PRT
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OTHER INFORMATION:
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US-08-714-741-47

US-08-152-488-10

US-08-152-488-11

US-08-303-025-11

US-08-303-025-11

US-08-303-025-11

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US-08-303-025-11

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US-08-677-304-13
US-08-436-703B-2
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Pred. No. 1.2e-16;
Mismatches 0;
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13, Appl
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22,853, Appl
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3: /cgn2_6/ptcdata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/1/iaa/FCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/1/iaa/backfiles1.pep:*

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Pred. No.

Minimum

DB seq

length:

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Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Searched:

Scoring table: Sequence: Title:

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Perfect score:

US-09-816-989A-2

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Total number of hits satisfying chosen parameters:

328717 seqs, 42310858 residues

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Result No.	Score	Query Match	Length	DB	ID	Description
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2		•	109	4	-09-405-743A-	e 7,
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σ.	120.5	56.6	66	4.	US-09-405-743A-4	4
7	108	50.7	35	4.	US-09-405-743A-1	,_
œ	91	42.7	223	w	1	e 201,
9	91	42.7	223	4.	US-09-205-426-201	Sequence 201, App
10	89.5	42.0	214	w	US-09-041-889-27	e 27,
11	89.5	42.0	214	4.	US-09-417-264-27	e 27,
12	86	40.4	407	4.	US-09-252-991A-29581	2958
13	78	36.6	316	4.	US-09-252-991A-32957	æ
14	77.5	•	700	4.	US-09-107-532A-5094	Sequence 5094, Ap
15	77	•	103	w	US-09-041-889-39	e 39,
16	77		103	4.	US-09-417-264-39	Sequence 39, Appl
17	77		116	w	9-	38,
18	77	•	116	4	US-09-417-264-38	Sequence 38, Appl
19	77	•	158	w	US-09-041-889-40	40,
20	77		158	4	US-09-417-264-40	40,
21	77		222	w	US-09-041-889-3	س -
22	77		222	w	US-08-837-058-3	ω -
23	77		222	4.	US-09-417-264-3	
24	77		226	w	US-09-041-889-32	Sequence 32, Appl
25	77		226	4	US-09-417-264-32	32,
26	75	35.2	8991	4	US-08-714-741-32	
27	74.5		32	_	US-08-152-488-13	13,

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US-09-405-743A-3
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LENGTH: 56
                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 5
LENGTH: 77
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Best Local
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CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
                                                                                                                                                                                                                                    LENGTH: 77
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: PEPTIDE
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Local Similarity 68.4%;
nes 39; Conservative
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   YKAEAAKAAAKEAAYEA
                                                             AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
                                                                                                                            Conservative
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76.6%;
                                                                                                                                           61.5%;
50.6%;
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                                                                                                                                         Score 131; DB 4;
Pred. No. 1.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 134.5; DB 4
Pred. No. 3.5e-08;
0; Mismatches 5
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                                                                                                                            Mismatches
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                                                                                                                                                          Length
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RESULT 7
US-09-405-743A-1
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US-09-405-743A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-09-405-743A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09405743A
Patent No. 6514938
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATS MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09405743A
Patent No. 6514938
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR
FILE REFERENCE: 60807-A
                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 6
LENGTH: 86
                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                  Query Match
Best Local
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Best Local Similarity 45.3%;
                                                                     Sequence 1, Application US/09405743A Patent No. 6514938
                                                                                                                                                                                                                                               Matches
                                                                   Patent No.
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REPERENCE: 60807-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/405,743A CURRENT FILING DATE: 1999-09-24 NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 66
                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                            29
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                                                                                                                                                                            AKKYAKAAKAE---KKEYAAAEAK----YKAEAAKAAAKEAAYEA
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                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                              56.6%;
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                                                                                                                                                                                                                                                 0; Mismatches
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Pred. No. 1.3e-06;
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Pred. No. 3.8e-07;
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                                                                                                                                                                                                                                                                                  DB 4;
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RESULT 8
US-09-095-855-201
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; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: PEPTIDE
US-09-405-743A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PASEQ ID NO 1
LENGTH: 35
TYPE: PRT
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Best Local :
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CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Prestidge, Ross
                                                                                                                                                                 NAME: Sleath, Janet REGISTRATION NUMBER: 37,007 REFERENCE/DOCKET NUMBER: 110 TELECOMMUNICATION INFORMATION: TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                   FILING DATE: 12-UN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Compounds and TITLE OF INVENTION: Treatment and
                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM CON OPERATING SYSTEM:
                                               TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                               TOPOLOGY:
                                                                                                                                                       TELEFAX: 206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                               ENGTH:
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Similarity 64.4%;
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2601 Elliott Avenue, Suite 4185
                                                                                   223 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tan,
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                                 linear
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               protein
                                            single
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Pred. No. 1.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methods for Diagnosis of Mycobacterial Infections
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US-09-041-889-27
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LENGTH: 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6033864
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Best Local Similarity
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EARLIER FILING DATE: 1996-08-29
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: 08/997,362
EARLIER FILING DATE: 1997-12-23
EARLIER APPLICATION NUMBER: 08/873,970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/205,426
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: 09/095,855
EARLIER FILING DATE: 1998-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Compounds and Methods for Treatment and
TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
FILE REFERENCE: 1100.1002c4
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER FILING DATE: 1997-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Mycobacterium vaccae
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FORM
COMPUTER: IBM FORM
COMPUTER: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
FILING DATE:
                                                                                                                                                                                                                                                                                                                           APPLICANT: Braun, Jonathan APPLICANT: Cohavy, Offer TITLE OF INVENTION: Diagnos TITLE OF INVENTION: Microbi
                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                       CITY: San Diego
STATE: California
                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 AKKAATKAAPAKKATAAKKAAPAKKATAAKKAAPAKKAPAKKAATKA 183
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                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                  Diagnosis, Prevention and Treatment Ulcerative Colitis, and Clinical Sub
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 91; DB 4;
Pred. No. 0.0062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 91; DB 3;
Pred. No. 0.0062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 223;
                                                                   #1.25
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                                                                                                                                                                                                                                                                                                                                                    Subtypes Thereof, Using
                                                                                                                                                                                                                                                                                                                                                                         ဝှု
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CLASSIFICATION: PRIOR APPLICATION DATA:

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RESULT 11
US-09-417-264-27
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; MOLECULE TYPE:
US-09-417-264-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
                                                                                                             TELEFAX: (619) 535-8949
NFORMATION FOR SEQ ID NO: :
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                  NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31.815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Diagnosis, Prevention and Treatment of TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using TITLE OF INVENTION: Microbial UC pANCA antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Braun, Jonathan APPLICANT: Cohavy, Offer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: P-PM 3006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Diego
STATE: California
                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 AKKVAKKAPAKKATKAAKKAATKAPA---RKAATKAPAKKAATKA 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                (619) 535-9001
             peptide
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                                                                                                                                                                                                                                                                                     US 09/041,889
                                                                                                               27:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 89.5; DB 3; Length 214; Pred. No. 0.0086; 4; Mismatches 13; Indels
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US-09-252-991A-32957
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US-09-252-991A-29581
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                                                                                                                                                                                                                                                                      ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32957
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Sequence 32957, Application.

Sequence 32957, Application.

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT:

MARC J. Rubenfield et al.

APPLICANT:

APP
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29581
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
SEQ ID NO 32957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                               Matches
                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 107196.135
FILE REFERENCE: 107196.135
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: 1998-02-18
CO/094.190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                             LENGTH: 316
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH: 407
                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 51.1
nes 24; Conservative
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nes 25; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 AQKAAEAKKADEAKKAAEAKAAEQKKQADIAKKRAEDEAKKKAAEDA 231
157
                                                                                                                               23;
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                                                        1 АККУАККАККАККАУКААБАККААКУЕКАААБКААКЕАА 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
AKKVAKKAPAKKATKAAKKAATKAPA---RKAATKAPAKKAATKA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                               36.6%;
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                                                                                                                                                               Score 78; DB 4; Length 316; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 86; DB 4,
Pred. No. 0.039,
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                                                                                                                                      19;
                                                                                                                                      Indels
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RESULT 14 US-09-107-532A-5094

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US-09-041-889-39
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APPLICATION NUMBER: US/09/107,532A
FILLING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILLING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILLING DATE: 1019 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELEPHONE: (781)893-5007
TELEPHONE: (781)893-5007
TELEPAX: (781)893-507
INFORMATION FOR SEQ ID NO: 5094:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5094, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCCOCCUS
                                                                               Sequence 39, Application US/09041889
Patent No. 6033864
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Microbial UC pANCA antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE:
STREET: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 53.7 es 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...700
SEQUENCE DESCRIPTION: SEQ ID NO: 5094:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Waltham
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YE: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                36.4%; Score 77.5; DB 4; Length 700; 53.7%; Pred. No. 0.55; ative 7; Mismatches 9; Indels
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FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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US-09-041-889-39
                                                                 Matches
                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/837
APTLING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                               TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO:
                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/041,889
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51 AKPKAKKAGAAKAKKPAGATPKKAKKAAGAKKAVKKTPKKAKKPAA 96
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52.2%;
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                                                                                Score 77; DB 3;
Pred. No. 0.088;
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                                                                                                  DB 3;
                                                                 13;
                                                                                                  Length 103;
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Search completed: January 21, 2004, 09:02:20 Job time: 8.47403 secs

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      GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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RESULT 2 F90725

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g V	g Qy	Query M Best Lo Matches	A;Gene: A;Map po A;Start C;Keywor F;14-34/ F;78-301 F;355-36	A; Mole A; Resi A; Cros A; Expe C; Comm	Scienc A;Titl A;Refe A;Acce A;Stat	A; Residues: A; Cross-refi A; Experiment A; Note: the R; Blattner, A; Rose,	R;Leve. J. Bac A;Titl A;Refe A;Acce A;Mole	RESULT JV0057 tolA p C;Spec C;Date C;Acce		33333333333333333333333333333333333333
56 AKKI 178 AAAI	1 AKKY :: 120 AEEA	Match ocal Simi	Gene: tola, Gene:	A, Molecule type: DNA A;Residues: 1-421 <blat> A;Cross-references: GB:AE000177; A;Experimental source: strain K-1 C;Comment: tolA and tolB proteins</blat>	Science 277, 1453-1462, 1997 A;Title: The complete genome ser A;Reference number: A64720; MUII A;Accession: B64810 A;Status: nucleic acid sequence	lues: 1-421 <lev> s-references: GB: rimental source: the authors tra ner, F.R.; Plunk se, D.J.; Mau, B</lev>	R; Levengood, S.K.; W J. Bacteriol. 171, 6 A; Title: Nucleotide: A; Reference number: A; Accession: JV0057 A; Molecule type: DNA	T 1 protein - Esc cies: Escheri ce: 07-Sep-190 cession: JV000		154.5 154.5 153.5 153.5 153.5 150 150 140 140 147 147
BAY-KAEA BAQKKAEA	AKKAE	36.5%; Similarity 53.0%; (1; Conservative 1	17 min FIG Leotide bi transmemb helical helical	s: DNA 121 <blat> nces: GB:AE000177; GB: source: strain K-12, and tolB proteins ar</blat>	-1462, 1 lete gen c: A6472 lo acid se	<pre><lev> : GB:M2 :rce: st rcs trans plunket fau, B.;</lev></pre>	Webste 6600-6 de seque C: JV005	Bscherichia coli erichia coli 1990 #sequence_re		22242222222222222222222222222222222222
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C;Becies: Bscherichia coli
C;Bete: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change
C;Accession: G85576
C;Accession: G85576
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner,
R;Perna, N.T.; Plunkett N.T.; Davis, N.W.; Lim, A.; Dimalanta, E.;
histone H1 - sea urchin (Lytechinus pictus)
C;Species: Lytechinus pictus (painted urchin)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988
C;Accession: A25550
R;Knowles, J.A.; Childs, G.J.
Nucleic Acids Res. 14, 8121-8133, 1986
A;Title: Comparison of the late H1 histone genes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:BA000007; PIDN:BAB34197.1; PID:g13360233; GSPDB:GN00154 A;Experimental source: strain O157:H7, substrain RIMD 0509952 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: F90725
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Hgasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                         RESULT 4
A25550
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A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85576
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A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: strain
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Matches 60
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;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics:
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s: Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKKYAKKAE----KAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAK-EAAK 55
                                                                                                                                                                                                                                                                                                  AEEAAKQAELKQKQAEEAAAKAAADAKAKAEADDKA--AEEAAKKAAADAKKKAEAEAAAK
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                                                                                                                                                                                                                        AAAEAQKKAEAAAALKKKAEAAEAAAAEARKKAAAEKAAADKKAAEKAAAEKAA
                                                                                                                                                                                                                                                         АККЕЛУ-КАБАККУЛКЛАКАБККЕУЛЛАБЛКК---ДЕЛЛКАУКАБЛАКАЛКЕЛЛ 106
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                                                                                                                                                                                                                                                                                                                                                                              Score 181.5; |
Pred. No. 4.7e
L2; Mismatches
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Pred. No. 4.7e-05;
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No. 4.7e-05;
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    the
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    urchins Lytechinus
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Potamousis,
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                                                                                   23-Jul-1999
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K.; Aş
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                                             A;Status: preliminary
      ;Molecule type: DNA
;Residues: 1-376 <PAR>
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C;Accession: E83525
R;Stover, C.K.; Pham, X.Q.; E.
adman, S.; Yuan, Y.; Brody, L
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;

A;Title: Complete genome sequence of a multiple drug resistant

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AG0592
                                                                                                                                                             tolA protein [imported] - Salmonella enterica subsp. enterica serovar C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov C;Accession: AG0592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Complete genome sequence of Pseudomonas aeruginosa A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: E83525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: A25550; MUID:87040778; PMID:3022245
A;Accession: A25550
A;Molecule type: DNA
A;Residues: 1-210 <KNO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE004530; GB:AE004091; NID:g9946865; PIDN:AAG04360.1; A;Experimental source: strain PAO1
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A;Molecule type: DNA
A;Residues: 1-347 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: tolA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: Pseudomonas aeruginosa
                                                                                                                                                  R;Parkhill, J.; Dougan, G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TolA protein PA0971 (imported) - Pseudomonas aeruginosa
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Similarity 50.0%;
58; Conservative
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                                                                                                                                                                                                                                                                                                                                                      A-EDBAKK--KAABDAKKK-AABDAKKKAABBAKKKAAVBA
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                                                                                                                           P.; Cronin,
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L.L.; (
                                                                                                                           James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Clin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 179; DB 2;
Pred. No. 6.2e-05;
7; Mismatches 29;
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Pred. No. 3.2e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.L.; Mizoguchi, S.D.; Warrener, Coulter, S.N.; Folger, K.R.; Kas,
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                                              Skelton, J.;
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K.; Lim,
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A;Cross-references:
C;Genetics:
A;Gene: STY0793
                                                                                                             R;Neesen, J.; Heinlein, U.A.O.; Buenemann, submitted to the EMBL Data Library, June 1 A;Reference number: $34153 A;Accession: $34153
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A; Cross-references:
C; Superfamily: neuro
                                                                      A; Molecule type: mRNA
A; Residues: 1-344 < NEE>
                                                                                                                                                                       mst101-1 protein - fruit fly (Drosophila hydei) C;Species: Drosophila hydei C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 C;Accession: S34153
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A; Residues: 1-388 < KUR>
                           C;Genetics:
A;Gene: FlyBase:Dhyd/mst101
                                                      A; Cross-references: EMBL: X73480; NID: g313199; PID: g313200
                                                                                               A;Status: preliminary
                                                                                                                                                                                                                                  S34153
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Best Local
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                                                                                                                                                                                                                                                                                                                        A 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKAAADAKKKAEAEAAKAAADAKKKAEAEA- AKAAADAKKKAEAEA---AKAAAEAKK--
nces: FlyBase:FBgn0011816
neurofilament triplet H ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.3%; Score 178; DB 2; 52.3%; Pred. No. 7.6e-05;
                                                                                                                                          Library, June 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 178; DB 2;
Pred. No. 7.8e-05;
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protein
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histone H1-beta, embryonic - sea urchin (Strongylocentrotus purpuratus) C;Species: Strongylocentrotus purpuratus (purple urchin) C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 23-Feb-1997 C;Accession: A28100 C;Accession: A28100 C;C;Childs, G.
                                                                                                                                                                                                                                                                                                                                                                                                          R;Neesen, J.; Padmanabhan, S.; Buenemann, H.
Eur. J. Biochem. 225, 1089-1095, 1994
A;Title: Tandemly arranged repeats of a novel highly charged 16-amino-acid motif represe lpha-helical rods within the extremely elongated spermatozoa of Drosophila hydel.
A;Reference number: S51364; MUID:95045538; PMID:7957199
A;Accession: S51364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-211 <LAI>
A;Cross-references: GB:M20314
C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; embryo; nucleosome; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOl. Cell. Biol. 8, 1842-1844, 1988
A,Title: Characterization of the structure and transcriptional patterns A,Reference number: A28100; MUID:88246461; PMID:2837660
A;Accession: A28100
                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-163,'E',164-236,'Q',237-254,257-320,'E',321-1390
A;Cross-references: EMBL:X73481; NID:g313201; PID:g313202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sperm tail-specific protein mst101(2) - fruit fly (Drosophila hydei)
C;Species: Drosophila hydei
C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C;Accession: S51364; S34154
                                                                                          A;Cross-references: FlyBase:FBgn0011816
                                                                                                                                                                                                                             A; Reference number: S34153
A; Accession: S34154
                                                                                                                                                                                                                                                                          R; Neesen, J.; Heinlein, U.A.O.; Buenemann, submitted to the EMBL Data Library, June 1
                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-1390 <NEE>
A; Cross-references: EMBL: X73481
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                                                                                                                                                                                                                                                                                                                                                                                          A; Status: nucleic acid sequence
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Best Local S
Matches 58
                                                                                                                  ;Gene: mst101(2)
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                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKEAAKAKKEAYKAEAKKYAKAAKAEKKEYAAAEAKK-AEAAKAYKAEAAKAAAKEAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKKEKEAAEKKKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEKKK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KPAAKKAKKPAAKKAAKKPAAKKPAAKKAAAKPAPAKKAAKKPAAKKAAKKVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KYAKKAE-KAYAKKAK--AAKEKKAYAKKEAKAYKAABAK-KKAKAEAKKYAKEAAK---
33.0%;
ilarity 46.2%;
Conservative 1
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48.7%;
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    11,
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  Score 171.5; DB 2;
Pred. No. 0.00051;
1; Mismatches 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 0.00011;
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                                                                                                                                                                                                                                                                          nemann, H.
June 1993
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                                             Length 1390;
       Indels
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       15;
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R;Kappe, S.H.I.; Noe, A.R.; Fraser, T.S.; Blair, P.L.; Adams, J.H. Proc. Natl. Acad. Sci. U.S.A. 95, 1230-1235, 1998
A;Title: A family of chimeric erythrocyte binding proteins of mala A;Reference number: Z16577; MUID:98115903; PMID:9448314
A;Accession: T09127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Parechinus angulosus (angulate urchin)
C;Date: 31-Mar-1980 #sequence revision 31-Mar-1980 #text_change 16-Feb-1997
C;Accession: A91090; A91091; A02586
R;Strickland, W.N.; Strickland, M.; de Groot, P.C.; von Holt, C.; Wittmann-Liebold, Eur. J. Biochem. 104, 559-566, 1980
A;Title: The primary structure of histone H1 from sperm of the sea urchin Parechinus rminal cyanogen bromide paptides.
A;Reference number: A91090; MUID:80156831; PMID:6767609
A;Contents: sequence of residues 1-84
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A;Note: 144-Arg was also found
C;Superfamily: histone H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 1-248 <STR>
A;Residues: 1-248 <STR>
A;Residues: 1-248 <STR>
B;Strickland, W.N.; Strickland, M.; Brandt, W.F.; von Holt, C.; Lehmann, A.; Wittmann-Li
R;Strickland, W.N.; Strickland, 1980
Eur. J. Biochem. 104, 567-578, 1980
A;Title: The primary structure of histone H1 from sperm of the sea urchin Parechinus and
A;Reference number: A91091; MUID:80156832; PMID:7363905
A;Accession: A91091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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                                                                                                                                                                                            A; Molecule type: DNA;
A; Residues: 1-1701 <KAP>
A; Cross-references: EMBL: AF031886; NID: 92947227;
A; Experimental source: subspecies yoelii; strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable erythrocyte-binding protein MAEBL - Plasmodium yoelii
C;Species: Plasmodium yoelii
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                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
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     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Plasmodium yoelii;Date: 11-Jun-1999 #text_change 11-Jun-1999;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999;Accession: T09127
                                                                                                   ;Introns: 62/1; 1648/1; 1674/2; 1697/1; Keywords: alternative splicing; cell
                                                                                                                                                      Gene: maebl
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                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA binding; nucleosome; sperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gonadal - sea urchin (Parechinus angulosus)
     Similarity 53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.9%;
32.9%; Score 170.5; DB 2
53.5%; Pred. No. 0.00068;
tive 11; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Mismatches
                                                                                           cell binding; erythrocyte invasion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 170.5; DB 1
Pred. No. 0.00017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                DB 2;
                                                                                                                                                                                                 PID: 92947228
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     Indels
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     Best Loc
Matches
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histone H1 - Chlamydomonas reinhardtii
(;Species: Chlamydomonas reinhardtii
(;Species: Chlamydomonas reinhardtii
(;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 23-Jul-1999
(;Accession: $59589; 862122
(;Accession: $59589; 862122
R;Fabry, S.; Mueller, K.; Lindauer, A.; Park, P.B.; Cornelius, T.; Schmitt, R.
curr. Genet. 28, 333-345, 1995
A;Title: The organization structure and regulatory elements of Chlamydomonas histone
A;Reference number: $59581; MUID:96120862; PMID:8590479
A;Accession: $59589
                                                                        A;ACCEBEACH.
A;ACOLECULE type: DNA
A;Residues: 1-173,'P',174-231 <FAW>
A;Residues: 1-173,'P',174-231 <FAW>
**Cross-references: EMBL:U16726; NID:g571479; PIDN:AAA98452.1; PID:g571480
                                                                                                                                                                                                                                                       A;Cross-references: EMBL:U16726
A;Note: the authors did not translate the codon for residue 1
A;Note: the authors did not translate the codon for residue 1
R;Fabry, S.; Ford, C.; Lindauer, A; Mueller, K.; Cornelius, T.; Schmitt, submitted to the EMBL Data Library, October 1994
A;Description: The organization, structure and controlling elements of Chl
A;Reference number: S62122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: A28456
R;Coles, L.S.; Robins, A.J.; Madley, L.K.; Wells, J.R.E.
J. Biol. Chem. 262, 9656-9663, 1987
A;Title: Characterization of the chicken histone H1 gene complement.
A;Reference number: A92655; MUID:87250632; PMID:3597432
A;Accession: A28456
C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; nucleosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-231 < FAB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: nucleic acid sequence not
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S59589
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C; Keywords: acetylated amino end; chromosomal protein; DNA binding; nucleosome; nucleus
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A; Residues: 1-220 < COL>
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C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 04-Mar-2000
                                                          A; Introns: 62/3; 101/3
                                                                                                                                                                                                                                   A; Accession: S62122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     v
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     АКАККВАУКАЕАККУАКЛАКАЕККЕУАА-АЕАККАЕААКАУКАЕААКАЛАКЕ 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKKPGEVKEKAPRKRTPAAKPKKPAAKKPASAAKKPKKAAAAKKSPKKAKKPAAAATKKA
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                                                                                                                                                                                                                                                                                                    controlling elements of Chlamydomonas
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Match 31.7%; Local Similarity 45.9%;

56;

Conservative

10; Mismatches Score 164.5; DB 2 Pred. No. 0.00038;

DB 2;

Length Indels

231; 17;

Gaps

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RESULT 15
S19113
Search completed: January 21, 2004, 09:01:40 Job time: 20.8182 secs
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C;Species: Chlamydomonas reinhardtii
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
C;Accession: S19113; S14466
R;Wakarchuk, W.W.; Mueller, F.W.; Beck, C.F.
Plant Mol. Biol. 18, 143-146, 1992
A;Title: Two GC-rich DNA elements of Chlamydomonas reinhardtii with complex arrangements A;Reference number: S19113; MUID:92119224; PMID:1731966
A;Accession: S19113
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                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: cgcr-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-265 <WAX>
                                                                                                                                                                                                                                                                                                                            Query Match 31.6%; Score 164; DB 2; Length 265; Best Local Similarity 39.4%; Pred. No. 0.00045; Matches 50; Conservative 21; Mismatches 38; Indels 18; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 KKAAKKAATPKKAAAPKKEGAVKKTKAPKKEGEKKPKSAKKAEKKPKKEGEKKKAAKPAK 159
                                                                                199 EAKAKEA 205
                                                                                                                         103 KEAAYEA 109
                                                                                                                                                                 139 RVAAEARAAAAAEARAAAAEAAAAAKARVAAEARAAAAAEARAAAAAAAAAKARAAA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 KAKKEAYKAEAKKYAKAA----KAEKKEYAAAE---AKKAEAAK---AYKAEAAKAAAKE 104
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Maximum Match 100%
Listing first 45 summaries
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rattus norv mycobacteri neurospora chironomus salmo trutt chironomus aedes aegyp chironomus oryctolagus homo sapien volvox cart homo sapien

ALIGNMENTS

701A protein TOLA OR CIM Bacteria; Pr Bacteria; Pr Enterobacter NCBI TaxID=5 [1] - TaxID=5 [1] - TaxID=5 [1] - TaxID=5 SEQUENCE FRO SEQUENCE FRO STRAIN=97105 MEDLINE=9712 Blattner F.R Filey M., Co Gregor J., Co Gregor J., Co Gregor J., Shao "The complet Science 277: Blattner F.R Riley M., Co Gregor J., Shao "The complet Science 277: Blattner F.R Riley M., Co Gregor J., Shao "The complet Science 277: Blattner F.R Riley M., Co Gregor J., Shao "The complet Science 277: Blattner F.R Riley M., Co Gregor J., Shao "The complet Science 277: Blattner F.R Riley M., Co Gregor J., Shao "The complet Science 277: Blattner F.R Riley M., Co STRAIN=1, A Ikemoto K., K Mori H., Mot Sampei G., S Yano M., Shao "Tola: a mem extended hel Proc. Natl. [5] DOMAINS- MEDLINE=9713 DEFOUNCE FRO "A 718-kb DN COLUMN RED. INTERACTION MEDLINE=9713 DEFOUNCE FRO "A 718-kb DN COLUMN RED. INTERACTION MEDLINE=9713 DEFOUNCE FRO "A 718-kb DN COLUMN RED. INTERACTION MEDLINE=9711	TOLA DT	ESI
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EMBL; AE000177; AAC73833.1;
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                                                                                                                                                                                                                                                                                                                Score 189.5; DB 1
Pred. No. 4.6e-06;
1; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PERIPLASMIC (POTENTIAL).

DOMAIN II (ALDHA-HELICAL).

DOMAIN III (FUNCTIONAL).

10 X TANDEM REPEATS OF [ED]-K(1,2)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ructure; Complete
CYTOPLASMIC (POTEN
                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                        8B2F52B4B97C655E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteriocin transport; Transmembrane;
                         210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce,
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                         8
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                                                                                                                                                                                                                                                                                                                                                            DB 1;
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                                                                                                                                                                                                                                                                                                                                                          Length
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                                                                                                                                                                                                                                                                                                                                                               421;
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                                                                                                                                                                                                                                                                                                                  11;
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RESULT
TOLA_PS
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01-JAN-1988 (Rel.
15-JUL-1999 (Rel.
Late histone H1.
                                                                                                                                                                                    TOLA_PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lytechinus pictus and Strongelocentrotus purpuratus.";
Nucleic Acids Res. 14:8121-8133(1986)
-1- FUNCTION: HISTONES HI ARE NECESSARY FOR THE CONDENSATION
NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lytechinus pictus (Painted sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleu
Echinoidea; Euechinoidea; Echinacea; Te
            SEQUENCE FROM N.A. STRAIN=PAO;
                                                                                                    Tola protein.
TOLA OR PA0971.
                                                                                                                                                           P50600;
01-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                   Chromosomal
SEQUENCE :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the SI the European Bioinformatics Institute. There are no resti
MEDLINE=97113525; PubMed=8955385;
                                                NCBI_TaxID=287;
                                                              Pseudomonadaceae;
                                                                            Bacteria; Proteobacteria;
                                                                                          Pseudomonas aeruginosa
                                                                                                                               16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00526; H15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro, IPR005818; Histone_H1/H5
InterPro, IPR005819; Histone_H5.
InterPro, IPR005216; Linkerh1st N.
Pfam; PF00538; linker_histone; T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X04488; CAA28177.1; -. PIR; A25550; A25550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Knowles J.A., Childs G.J.; "Comparison of the late H1 histone genes of the sea urchins "Comparison of the late H1 histone genes of the sea urchins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=87040778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7653;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lytechinus.
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SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
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                                                                                                                                                                                                                                                                                                            KTEAQKA-RAAAKKAKLAAKKKEQKEKKAAKTKARKEKLAAKKAAKKAAKKVKKPAAKAK
                                                                                                                                                                                                                                                                                                                                     ККУАККАЕКАУАККАКААКЕККАУАККЕАКАУКААЕ---- АКККАКАЕАККУАКЕААКАК
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(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                   protein; Nuclear protein; DNA-binding; Multigene family.
210 AA; 21746 MW; 08C38F64894007E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                       STANDARD;
                                                                                                                                40,
40,
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                                                                           Gammaproteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                 80
                                                                                                                                                                                                                                                                                                                                                             Score 181; DB 1;
Pred. No. 9.3e-06;
8; Mismatches 36
                                                                                                                                                                                       PRT;
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a; Temnopleuroida; Toxopneustidae;
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http://www.isb-sib.ch/announce/
                                                                               Pseudomonadales;
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Best Local Similarity
Matches 54; Conser
                                                                                                                                                                                                                                                          DROHY
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren Hickey M.J., Brinkman F.S.L., Hufinagle W.O., Kowalik D.J., Ling Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yu Brody L.L., Coulter S.N., Folger K.R., Kas A., Latbig K., Ling Brody L.L., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen."; Nature 406.959-964(2000).
                                                                                                                                                                                                                                    MST1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. The state content is in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                    Drosophila hydei (Fruit fly)
                                                                                          Axoneme-associated MST101(1).
                                                                                                                                     01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                      Q08695;
01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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InterPro; IPR006260; TonB C.
TIGRFAMs; TIGR01352; tonB_Cterm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U39558; AAC44660.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
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MEDLINE=20437337; Po
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J. Bacteriol. 178:7059-7068(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dennis J.J., Lafontaine E.R., Sokol E "Identification and characterization"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS
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E83525; E83525.
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t annotation
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Pred. No. 1.
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PERIPLASMIC (POTENTIAL).
POLY-ALA.
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D.J., Lagrou M.,
n S., Yuan Y.,
K., Lim R.M.,
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                                                                                                                                                                                                                                                                                                                                                    204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
MST2_DROHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995
01-FEB-1995
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MST2_DROHY
Q08696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The Drosophila hydei gene Dhmst101(1) encodes repetitive, axoneme-associated protein with dif Y chromosomal deletion mutant flies.";

Dev. Biol. 162:414-457:70004
                                                                                             "Tandemly arranged repeats of a novel highly charged 16-amino-acid motif representing the major component of the sperm-tail-specific axoneme-associated protein family Dhmst101 form extended alpha-helical rods within the extremely elongated spermatozoa of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/amor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                               Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: POSSIBLE STRUCTURAL ROLE IN 1
ASSOCIATED WITH AXONEMAL STRUCTURES.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By 6
-!- TISSUE SPECIFICITY: TESTIS. LOCATED IN
                                                                          Drosophila hydei.";
                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND CHARACTER MEDLINE=95045538; PubMed=7957199;
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda;
                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila hydei (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                       MST101(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sperm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.,
TISSUE=Testis;
                                                                                                                                                                                                       Neesen J., Padmanabhan S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Axoneme-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0011816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94200512; PubMed=8150205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPERMATID BUNDLES.

DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
POLYMORPHISM: THE NUMBER OF REPEATS VARIES BETWEEN
                          FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; X73480; CAA51;
S34153; S34153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 AKEAAKAKKEAYKAEAKKYAKAAKAEKEYAAAEAKK-AEAAKAYKAEAAKAAAKEAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat; Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58,
                                                     Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAEAAKKEKEA--AEKKKCAEAAKKEKE---AAEKKKCAEAAKKEKEAAEKKKCAEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKKYAKKAEK----AYAKKAKAAKEKKAYAKKEAKAYKAAE------AKKKAKAEAKKY 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKKEKEAAEKKKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEKKK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162:414-425(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 (Rel.
6 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAA51875.1;
                          em. 225:1089-1095(1994).
POSSIBLE STRUCTURAL ROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31, Created)31, Last sequence update)40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein mst101(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37793 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND CHARACTERIZATION
                                                                                                                                                                                                                                                       AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  family.
Cytoplasmic.
                                                                                                                                                                                                       Buenemann H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 175.5; DB 1;
Pred. No. 3.1e-05;
3; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 X 16 AA APPROXIMATE TANDEM REPEATS K-K-K-C-X-E-X-A-[KQ]-K-X-X-E-X-A-X.
                                                                                                                                                                               a novel highly charged 16-amino-acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24C65D2510387E2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     Hexapoda; Insecta; Pterygota;
                          ROLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1391 AA
                          Ä
                             BHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
N SPERMATOCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THE SPERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  des a testis-specific, differential abundanc
                             SPERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BETWEEN STRAINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
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RESULT 6
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Best Local S
Matches 54
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P02256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986
21-JUL-1986
15-JUL-1999
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PIR; §
                                                                                                                                                                                     Strickland W.N., Strickland M., Wittmann-Liebold B.;
                                                                                                                                                                                                                                                                                                                                 "The primary structure of histone H1 from sperm of the sea urchin Parechinus angulosus. 1. Chemical and enzymatic fragmentation of protein and the sequence of amino acids in the four N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-84,
MEDLINE=80156831; PubMed=6767609;
Strickland M.N., Strickland M., de
Wittmann-Liebold B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn02073; Dhyd\mst101(2).

Sperm; Repeat; Multigene family; Polymorphism.

Sperm; Repeat; Multigene family; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified
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                                                                                                   the entire primary structure.";
Eur. J. Biochem. 104:567-578(1980)
                                                                                                                                            "The primary structure of histone Parechinus angulosus. 2. Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=7658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Echinoidea; Euechinoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Histone H1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities
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                                                                                                                                                                                                                                                 SEQUENCE OF
                                                                                                                                                                                                                                                                                                                  cyanogen bromide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parechinus
                                                                                                                                                                                                                          MEDLINE=80156832; PubMed=7363905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN Buropean Bioinformatics Institute. There are no restr
                                                          . J. Biochem. 104:567-578 (1980).
FUNCTION: HISTONES H1 ARE NECESSARY
NUCLEOSOME CHAINS INTO HIGHER ORDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL. POLYMORPHISM: LENGTH POLYMORPHISMS EXIST BETWEEN DI STRAINS, MOST LIKELY CAUSED BY LENGTH VARIATIONS WI
                 SUBCELLULAR LOCATION:
TISSUE SPECIFICITY: SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1128
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  SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       x73481; CAA51876.1; -. S51364; S51364.
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                                                                                                                                                                                                                                                                                             Biochem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         АКЕЛАКАККЕЛУКЛЕЛККУАКЛАКАЕККЕУАЛАЕЛККАЕЛАКАУКЛЕЛАКАЛАКЕЛА 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKKYAKKAEKAY----AKKAKAAKEKKAYAKKEAKAYKAAE-----AKKKAKAEAKKY 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          angulosus (Angulate sea urchin).
Metazoa; Echinodermata; Eleutherozoa;
Euechinoidea; Echinacea; Echinoida; !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIFICITY: TESTIS. PRIMARY SPERMATOCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1391 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                    80-248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gonadal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                          peptides.";
104:559-566(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159000 MW;
SPERM.
TO THE HISTONE H1/H5 FAMILY
                                           Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 171.5; DB 1; Pred. No. 0.00017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      de
                                                                                                                                                                                                        Brandt W.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1B2A368F30F48878 CRC64;
                                                                                                                                            c H
                                                                                                                                                                                                                                                                                                                                                                                                                   Groot P.C.,
                                                                                                                                              from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248
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                                                            FOR THE CONDENSATION STRUCTURES.
                                                                                                                                            m sperm of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                           TON
                                                                                                                                                                                                                                                                                                                                                                                                                   von Holt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Echinidae;
                                                                                                                                                                                                        Holt C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1391;
                                                                                                                                                             the
                                                                                                                                                CNBr
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                                                                                                                                                               sea urchin
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                                                                                                                                            peptide
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                                                                                                                                                                                                           Lehmann
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InterPro; IPR005819; Histone_H5.
InterPro; IPR005216; Linkerhist N.
Pfam; PF00538; linker_histone; I.
PRINTS; PR00624; HISTONEH5.
PRODOm; PD000373; Linkerhist_N; 1.
SMART; SM00526; H15; 1.
                                                                                                                                                                                                                                                                                                                                  entities re
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P15869;
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VARIANT
                                                                                            InterPro; IPR005818; Histone_H1/H5
InterPro; IPR005819; Histone_H5.
InterPro; IPR005819; Histone H5.
InterPro; IPR005216; Linkerh1st N.
Pfam; PF00538; linker histone; I.
PRINTS; PR00624; H;5T0NEH5.
                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstating the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last seque)
15-JUL-1999 (Rel. 38, Last annot)
Histone H1-beta, late embryonic
                                                                                                                                                                                                                              EMBL; M20314; AAA30052.1; -. PIR; A28100; A28100. HSSP; P02259; 1HST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lai Z.-C., Childs G.;
"Characterization of the structure the gene encoding the late histone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=88246461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strongylocentrotus.
NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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HSSP; P02259; 1HST.
                                                    SMART; SM00526; H15;
                                                                          ProDom; PD000373; Linkerhist_N;
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                                                                                                                                                                                                                                                                                                                                     requires a license agreement (S
an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14, Last sequence update)
38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=2837660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.9%;
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     22169
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Nuclear protein; DNA-bindir
22169 MW; 9F214581334BBE7A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nuclear protein;
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                                                                                                                                                                                                                                                                                                                                                               agreement (See
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Pred. No. 5e-05;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      × - ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and transcriptional patterns of subtype H1-beta of the sea urch
     DNA-binding; Multigene
81334BBE7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA-binding; Multigene family;
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                                                                                                                                                                                                                                                                                                                                                               http://www.isb-sib.ch/announce/
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MBL outstation -
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Aldams M.D., Celniker S.E., Hichards S. Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S. Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S. Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Barlar D., Barlar D., Barlar D., Baldwin D., Ballew R.M., Basu A., Baxendale J., Baraktaroglu L., Beasley E.M., Ra Ballew R.M., Basu A., Baxendale J., Baraktaroglu L., Beasley E.M., RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bothakov S.M., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Brottier P., Cadley S., Dahlke C., Davenport L.B., Daviss P., Charly S., Dahlke C., Davenport L.B., Daviss P., Charly S., Calley S., Dahlke C., Davenport L.B., Daviss P., Park Charly J.M., Charly S., Dahlke C., Paerraz C., Ferriera S., Pleisohmann W., Roder K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Poller R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Ra Duzbin K.J., Barrishan A.E., Gazg N.S., Gelbart W.M., Glasser K., Ra Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Lai Z., Ling Y., Lin X., Lako P., Lei Y., Marthay T.C., McDarry C., Morris J., Moshrefi A., Mount S.M., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Melson K.A., Naton K.A., Nixon K., Nusskern D.R., Paclab J.M., Ra Allaris M.P., Nelson K.A., Sampan N., Sungskern D.R., Paclab J.M., Nelson K.A., Naton K., Nusskern D.R., Paclab J.M., Nelson K.A., Sungson M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAU
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STRAIN=Canton-S; TISSUE=Head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anoxia upregulated protein. FAU OR CG6544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9VGX3; Q95S18; Q9VGX1; Q9VGX2; Q9Y0F9; 
28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20196006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ma E., Xu T., Haddad G.G.; "Gene regulation by O2 deprivation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99097004; PubMed=9878744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phila melanogaster.";
Res. Mol. Brain Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148
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nilarity 48.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brain Res. 63:217-224(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 169.5; DB 1
Pred. No. 5.1e-05;
8; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fly).
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EMBL; AP154418; AAD38397.1; --
EMBL; AE003688; AAF54550.1; --
EMBL; AE003688; AAF54550.1; --
EMBL; AE003688; AAF54551.1; --
EMBL; AE003688; AAF54552.1; --
EMBL; AV060997; AAL28545.1; --
EMBL; AV119569; AAM50223.1; --
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Zheng X.H.,
Gibbs R.A.,
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Lewis S.E.
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                                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22426066; PubMed=12537569;
Stapleton M., Carlson J.W., Brokstein P., Yu
George R.A., Guarin H., Kronmiller B., Pacleb
Rubin G.M., Celniker S.E.;
"A Drosophila full-length cDNA resource.";
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The
                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                            Alternative splicing.
DOMAIN 88 143
DOMAIN 354 668
VARSPLIC 26 131
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GO; GO:0006979; P:response
                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q9VGX3-5; Sequence=VSP_004052;
-!- TISSUE SPECIFICITY: Concentrated in lamina neurons, lobe neurons and cortical neurons of central brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVISIONS, AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                          INDUCTION: By anoxia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yeh R.-F., Zaveri J.S., Zhan M., Zhang G., g X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., s. R.A., Myers E.W., Rubin G.M., Venter J.C., genome sequence of Drosophila melanogaster.", nce 287:2185-2195 (2000).
                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboratic een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9VGX3-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q9VGX3-3;
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ALA/GLU-RICH.

YPSVEKVTRYYKSYPIYSSYSVPRRVYGATRVVTSPIRVV
TSPARVVSRUHSPSPVRVVRTTTRVISSPERTTYSYTTPS
TYYSPSYLPSTYTSTYIPTSYTTY -> TPRLDLCTDRPGS
HRSRASSDYSYTSKSSVEKSSYDSSNPHSYRPERSTYTSTV
EKTSRSGPGGSYNYSTERTSTTGAGPGGYSYSSTTTSGNLPG
                                                                                              THR-RICH
                                                                                                                          oxidative
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Pacleb J.M.,
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                                                                                                                          stress;
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Best Local S
Matches 55
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P08286;
01-AUG-1988
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15-JUL-1999 (Rel. 38, Last annotation update)
Histone H1.10 (Methylated DNA binding protein-2-H1) (MDBP-2-H1).
Gallus gallus (Chicken).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasian
                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=87250632; PubMed=3597432;

Coles L.S., Robins A.J., Madley L.K., Wells J.R.E.;

Characterization of the chicken histone H1 gene complement.

Generation of a complete set of vertebrate H1 protein sequen

J. Biol. Chem. 262:9656-9663(1987).
             Schwarz S., Hess D., Jost J.P.;
"The methylated DNA binding protein-2-H1 (MDBP-2-H1) consists histone H1 subtypes which are truncated at the C-terminus."; Nucleic Acids Res. 25:5052-5055(1997).
-I- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION ON NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1988 (Rel.
01-NOV-1997 (Rel.
15-JUL-1999 (Rel.
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                                                                                                                                                MEDLINE=98060905; PubMed=9396815;
SUBCELLULAR LOCATION: Nuclear
                                                                                                                                                                                                                                                                                                                                                                          _TaxID=9031;
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#issing (In isoform B).
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YKSSYPIYSSYSVERRVYGATRVVTSPIRVVTSPARVVSRV
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TSPARVVSRVIHSPSPVRVVRTTTRVISSPERTTYSYTTPS
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RESULT 10
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Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                          Yelton D.B., Limberger R.J., Curci K., Malinosky-Rummell Sliviensky L., Schouls L.M., van Embden J.D., Charon N.W. "Treponema phagedenis encodes and expresses homologs of t pallidum TmpA and TmpB proteins.";
Infect. Immun. 59:3685-3693(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0624; HISTONEHS. SMART; SM00526; H15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents
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             EMBL; M58563; AAA27480.1;
                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                           Bacteria;
                                                                                                                                                                                                                                                                                                                           Treponema phagedenis.
Bacteria; Spirochaetes;
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InterPro; IPR005819; Histone_H5.
Pfam; PF00538; linker_histone; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M17018; AAA48788.1; -. HSSP; P08287; 1GHC.
 PIR; B43592; B43592
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                                                                                                                                                                                                                                                            MEDLINE=91372983; PubMed=1894368;
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                                                                                                                                                                                                                                                                                                                                                               reponemal
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    -!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.

                                                                                                                                                                                FUNCTION: TMP MAY SERVE
                                                                                                                                          SIMILARITY: TO TMPB OF T. PALLIDUM.
                                                                                                                                                        SUBCELLULAR LOCATION:
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219 AA;
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Last annotation updat
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Pred. No.
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                                                                                                       collaboration -
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RESULT 11
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REPEAT
                                                                SEQUENCE FROM N.A.

MEDILINE=87250632; PubMed=3597432;

Coles L.S., Robins A.J., Madley L.K., Wells J.R.E.;

Coles L.S., Robins A.J., Madley L.K., Wells J.R.E.;

"Characterization of the chicken histone H1 gene complement.

Generation of a complete set of vertebrate H1 protein sequently.

Biol. Chem. 262:9656-9663(1987).
                                                                                                                                                                                   01-AUG-1988
01-AUG-1988
                                                                                                                                                                                                   H11L_CHICK
P08287;
                                                                                                                                                                                                                    CHICK
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       MEDLINE=94032251; PubMed=8218199;
Cerf C., Lippens G., Muyldermans S., Segers A., Ramakrishnan V.,
Wodak S.J., Hallenga K., Wyns L.;
"Homo- and heteronuclear two-dimensional NMR studies of the globular
domain of histone H1: sequential assignment and secondary
                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                         Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                              REPEAT
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domain of histone H1:
structure.";
                                                                                                                                          Archosauria; Aves;
                                                                                                                                                                  Histone H1
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                                                                                                                                         Neognathae; Galliformes;
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POTENTIAL.
TREPONEMAL MEMBRANE PROTEIN B.
17 X 5 AA TANDEM REPEATS OF K-A-A-[AKR]-
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                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                          Phasianidae; Phasianinae;
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NUCLEOSOME CHAINS INTO HIGHER ORDER SUBCELLULAR LOCATION: Nuclear. SIMILARITY: BELONGS TO THE HISTONE!

HISTONE H1/H5 FAMILY

(Salmo

gairdnerii).";

FOR THE CON

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RESULT 12
H1_ONCMY
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Matches 49
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P06350;
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SEQUENCE
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INIT_MET
MOD_RES
                                                                                                    Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleost
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8022;
                            Mezquita J., Connor W., Winkfein R.J., I "An H1 histone gene from rainbow trout (J. Mol. Evol. 21:209-219(1985).
-I- FUNCTION: HISTONES H1 ARE NECESSARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochemistry 32:11345-11351(1993).

-I- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-I- SUBCELLULAR LOCATION: Nuclear
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                                                                         SEQUENCE FROM N.A. MEDLINE=85264847; PubMed=6443128;
                                                                                                                                                               Histone H1.
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15-JUL-1999
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InterPro; IPR005819; Histone_H5.
Pfam; PP00538; linker_histone; 1.
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PDB; 1GHC; 3
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49; Conser
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No. 0.00014;
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RESULT 13
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Best Local S
Matches 52
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P16401; Q14529;
01-AUG-1990 (Rel. 15, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
Histone H1.5 (Histone H1a).
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                                                    SEQUENCE FROM N.A.

MEDLINE=22296985; PubMed=12408966;

Marzluff W.F., Gongidi P., Woods K.R., Jin

"The human and mouse replication-dependent

Genomics 80:487-498(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                       Ohe Y., Hayashi H., Iwai K.;
"Human spleen histone Hl. Isolation
minor variants, Hla, Hlc, and Hld.";
J. Biochem. 106:844-857(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00526; H15; 1.
Chromosomal protein; Nuclear
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                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=97183654; PubMed=9031620;
Albig W., Meergans T., Doenecke D
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Mammalia; Eutheria;
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InterPro; IPR005819; Histone_H5.
Pfam; PF00538; Linker histone; 1.
PRINTS; PR00624; HISTONEH5.
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Pred. No. 0.
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Best Local Similarity
smegmatis.";
Mol. Gen. Ge:
-!- FUNCTION
                                                                                                                                                                                                                                                                                                                                                      Q9ZHC5;
16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD RES
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                 SEQUENCE FROM N.A.
STRAIN-ATCC 700084 / mc(2)155;
MEDLINE=99110209; PubMed=9894918;
Lee B.H., Murugasu-Oei B., Dick T
"Upregulation of a histone-like p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wild A.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: HISTONES HI ARE NECESSARY FOR THE CONDENSATION
NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0624; HISTONEH5.
SMART; SM00526; H15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005718; C:nucleosome; NAS.
GO; GO:0003677; F:DNA binding activity; NAS.
GO; GO:0007001; P:chromosome organization an
GO; GO:0006334; P:nucleosome assembly; NAS.
InterPro; IPR005818; Histone H1/H5.
InterPro; IPR005819; Histone H5.
Pfam; PF00538; linker histone; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z98744; CAB1142
PIR; S51660; S51660.
HSSP; P08287; 1GHC.
                                                                                                                                                                                                        NCBI_TaxID=1772;
                                                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteridae; Actino
Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 142711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC:4719; HIST1H1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF531304;
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                                                                                                                                                                                                                                                                                    Mycobacterium
                                                                                                                                                                                                                                                                                                            HUP OR HLP
                                                                                                                                                                                                                                                                                                                                DNA-binding
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INIT MET
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SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
    FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYCSM
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  Genet. 260:475-479(1998)
ION: THIS PROTEIN BELONGS
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225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein; Nuclear
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(Rel.
(Rel.
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40, Last sequence update)
40, Last annotation update)
vin HU homolog (Histone-like
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7; Mismatches
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MISSING (IN REF. 1).
, 26CD4A1E5D463CDA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organization and biogenesis (sen. .
                                                                      c T.;
protein
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                                                                           dormant
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                                                                                                                                                                                                                                                                                                                                  protein)
       LIKE FAMILY
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                                                                           Mycobacterium
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RESULT 15
H11R_CHICK
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01-AUG-1988
15-SEP-2003
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the Euro
                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@@isb-sib.ch).
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PROSITE; PS00045; HISTONE LIKE; 1.

DNA-binding; DNA condensation; Repeat.

BACTERIAL HISTONE-LIKE DOMAIN.

DOMAIN

101 205 DEGENERATE REPEATS REGION.

CARPET77F61F7EF09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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Pfam; PF00216; Bac DNA binding; 1.
ProDom; PD000945; Bac DNAbind; 1.
SMART; SM00411; BHL; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF068138; AAD13809.1; -. HSSP; P02346; 1HUU.
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EMBL; M17020;
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SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
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(Rel. 08, Last seq
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AAA48790.1;
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Pred. No. 0.00021;
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InterPro; IPR005819; Histone_H5.
Pfam; PF00538; Linker histone; 1.
PRINTS; PR00624; HISTONEH5.
SMART; SM00526; H15; 1.
                                                                                                                                                  INIT MET
                                                                                                                                     SEQUENCE
                                                                                                                                                                       3D-structure.
                                                                                                                                                                                   Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
                                                                                                                                                                                                                                                      PDB; 1GHC;
                                                                                                   Local Similarity
                                            109
169
                     58
                                                                                         52;
                                                                  1 AKKYAKKAEKAYAKKAKAAKEKKAYAKK---EAKAYKAAEAKKKAKAEAKKYAKEAAKAK 57
КЕАУКАЕАК-КУАКААКАЕККЕУАА-АЕАККАЕААКАУКАЕААКААКЕ 104
                                            SKKPGEGLEKAPKKKASAAKPKKAAAKKPAAAAKKPKKAVAVKKSPKKAKKPAASATKKS
                                                                                                                                     218 AA;
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                                                                                       Conservative
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                                                                                                                                     21672 MW;
                                                                                                  30.7%;
                                                                                      ; Score 159.5; DB 1; Pred. No. 0.00023; 11; Mismatches 41
                                                                                                                                                  GLOBULAR
                                                                                                                                     CB9724BFF14654A6 CRC64;
                                                                                                               DB 1;
                                                                                         41; Indels
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Search completed: January 21, 2004, Job time: 15.8636 secs 09:00:59

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Post-processing: Minimum Match 0%
Maximum Match 100%
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Maximum DB seq length: 2000000000
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Perfect score:
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   SPTREMBL 23:*

1: sp_acteria:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_numan:*

5: sp_invertebrate

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_vortebrate

13: sp_vertebrate

14: sp_urclassifit

15: sp_bacteriap:*

16: sp_archeap:*
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519
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                     sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_phage:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Q84528 paramecium	Q39598 chlamydomon	O01395 drosophila	Q39576 chlamydomon	O61164 plasmodium	Q9cm70 pasteurella	Q8xvn7 ralstonia s		Q8zgz2 yersinia pe	Q8z8c1 salmonella	Q8x965 escherichia	Q8zqt6 salmonella	Q8fjt1 escherichia	Q8t5c8 plasmodium	Q9wwxl pseudomonas	Q937k4 erwinia chr	Description

45	44	43	42	41	40	39	38	37	36	35	34	3	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
148.5	148.5	150	150	151	152	153.5	154	154.5	154.5	156	156	157.5	158	158	158	158.5	160.5	161	161.5	161.5	161.5	161.5	161.5	161.5	161.5	162	162.5	163
28.6	28.	28.9	28.	29.	29.	29	29.7				30.1								31.1	31.1	31.1	31.1	31.1			31.2	31.3	31.4
319	275	288	243	607	156	369	293	755	309	885	224	155	1341	290	281	298	301	296	306	297	295	295	295	295	293	356	1128	182
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Q8dam4 vibrio vuln	Q9xhl9 triticum ae		Ω	Q9v6s7 drosophila	Q8p6u0 xanthomonas												_		lathy	ש		lathy	Q81ki0 pisum sativ				Q26947 trypanosoma	Q45370 bordetella

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Best Local S
Matches 59
                                                                                                                 Q8T5C8;
01-JUN-2002
01-JUN-2002
01-OCT-2002
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SEQUENCE
Plasmodium vivax.
Eukaryota; Alveolata;
NCBI_TaxID=5855;
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InterPro; IPR006260; TonB C.
PRINTS; PR00624; HISTONEH5.
TIGRPAMS; TIGR01352; tonB Cterm; 1.
SEQUENCE 372 AA; 40133 MW; 8784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96422022; PubMed=8824639; Rodriguez-Herva J.J., Ramos J.; "Characterization of an OprL null mutant J. Bacteriol. 178:5836-5840(1996). EMBL; X74218; CAB50780.1; -..
                                                                             MAEBL.
                                                                                                                                                                                                            Q8T5C8
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Rodriguez-Herva J.J., Ramos Gonzalez M.I., Ramos J.;
"The Pseudomonas putida peptidoglycan-associated outer membrane
lipoprotein (PAL) is involved in maintenance of the integrity o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003
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Submitted (JUL-1999)
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                                                                                                                                                                                                                                                                                                                         KKAAAEEAKKKAAEDAKKKAAEEAKKKAAEDAKKKAAAEDAKKKAAEEAKKKAAADA 233
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| (JUN-1995)
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Pred. No. 6.3e-06;
4; Mismatches 31
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                            Haemosporida;
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                              Plasmodium
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RESULT 5
Q8ZQT6
ID Q8ZQ
AC Q8ZQ
DT 01-M
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ID Q8FJ
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Best Local Similarity
Matches 61; Conserv
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=Salvador;
STRAIN=Salvador;
Michon P., Stevens J.R., Kaneko O., Adams J.H.;
Mi
Q8ZQT6
Q8ZQT6;
01-MAR-2002
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Q8FJT1;
01-MAR-2003
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Bacteria; Proteobacteria;
Enterobacteriaceae; Esche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-O6:H1 / CFT073 / ATCC 700928;

MEDLINE=22388234; PubMed=12471157;

MEICH R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

Welch R.A., Burland V., Plunkett G. III, Redford P., Stroud
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOLA OR C0818.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002)
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01-MAR-2003
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421 AA;
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                                                                                                                                                                                                                                            ABEAAKQAELKQKQAEEAAAKAAADAKAKAEADAKA--AEEAAKKAAADAKKKAEAEAAK
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                                                                                                                                                                                                                                                                                                                                                                                                                          43184 MW;
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Pred. No. 9.6e-06;
1; Mismatches 32
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STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
Mayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoy,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe '
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunau
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
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MEDLINE-21534948; PubMed=11677609;

McClelland M., Sanderson K.E., Spieth J., Clifton S.W.,

Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou

Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., M
                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=0157:H7 / R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
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STRAIN=0157:H7 / E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
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Bscherichia coli O157:H7.
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01-OCT-2002 (TrEMBLrel.
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01-MAR-2002
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EMBL; AE008730; AAL19691.1; -.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete genome sequence of Salmonella enterica serovar Typhimurium
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    20, Last sequence update)
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Pred. No. 1.
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                                                                                                        K., Yokoyama K.,
M., Tobe T.,
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S., Layman D.,
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AC Q8ZG
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OBZEE

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SEQUENCE
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Churcher S., Basham D., Brooks K., Chillingworth T., Connerton P., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413.848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000104; Antifreeze_1.
PRINTS; PR00308; ANTIFREEZEI.
Complete proteome.
SEQUENCE 394 AA; 40517 MW; 5B58D8E8230BDE28 CRC64;
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EMBL; AE005252; AAG55075.1; -.
EMBL; AP002553; BAB34197.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CT18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella typhi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8Z8C1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8Z8C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                        137
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376 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                         <u>АККҮАККАЕҚАҮАКҚАҚААКЕКҚАҰАККЕАКАҰҚААЕАККҚАҚАЕАККҮАКЕААҚҚҚЕА</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>AAAEAQKKAEAAAAALKKKAEAAEAAAAEARKKAAAEKAAADKKAAEKAAAEKAA</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               АККЕАУ-КАЕАККУАКААКАЕККЕУАААЕАКК---АЕААКАУКАЕААКАААКЕАА 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEEAAKQAELKOKOAEEAAAKAAADAKAKAEADDKA--AEEAAKKAAADAKKKAEAEAAK
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                                                                                                                                                                                                                                                                                                  ҮКАЕАККҮАКААКАЕККЕҮАААЕАККАЕААКАҮКАЕААКААА---КЕААҮЕ 108
                                                                                                                                                                                                                                                                                                                                                        AKAAADAKKKAEAEAAKAAADAKKKAEAEA-AKAAADAKKKAEAEA---AKAAAEAKK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38804 MW;
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52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.3%; Score 178; DB 16;
52.3%; Pred. No. 4.5e-05;
tive 10; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220,
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Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EC21F2C4767A8A42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
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Q8ZGZ2; Q8ZGZ2; 01-MAR-2002 01-MAR-2002 01-MAR-2003

(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.

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Created) Last seq Last ann

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PRELIMINARY

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RESULT
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Matches 63
                                                      Query Match
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Matches 63
                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN-KIM5 / Biovar Mediaevalis;

MEDLINE-22137863; PubMed=12142430;

MEDLINE-22137863; PubMed=12142430;

Deng W., Burland V., Plunkett G. III, Boutin A., M.

Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.

Petraevan J.D., Lindler L.E., Brubaker R.R., Plan

Straevan D.C., McDonough K.A., Nilles M.L., Matson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CO-92 / Biovar Orientalis;
MEDLINE=21470413; PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Parkhill J., Wren B.W., Thomson N.R., Churcher C., Mungall K.L.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Leather S., Moule S., Oyston P.C.F., Whitchead S., Barrell B.G.,
Simmonds M., Skelton J., Stevens K., Whitchead S., Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 388 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                              Membrane spanning TOLA OR Y3056.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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TOLA OR YPO1123.
                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                         Yersinia pestis.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Yersinia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yersinia pestis
                                                                                                                                        "Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
EMBL; AE013906; AAM86606.1;
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Nature 413:523-527(2001).
EMBL; AJ414146; CAC89966.1; -.
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                                                                            Similarity
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AAAKKQA-DADAKKAVEVAEKAAADAAEKKAAADAE-KKAAAAKKVAAAAEAKKKAAAEA
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                                                      Conservative
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                                                                                                                          41012 MW;
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                                                          12;
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                                                      Score 178; DB Pred. No. 4.7e. 2; Mismatches
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Pred.
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                                                        .7e-05;
les 28;
                                                                                           DB 16;
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                                                                                         Length 393;
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                                                          Indels
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                                                          18;
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                                                          Gaps
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RESULT 11
Q9CM70
ID Q9CM7
AC Q9CM7
AC Q9CM7
DT 01-U1
DT 01-O1
DT 01-O2
DB T01A
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Best Local S
Matches 67
                                                                                 Q9CM70;
Q9CM70;
01-JUN-2001
01-JUN-2001
01-OCT-2002
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Q8XVN7;
Q1-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                  Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum.", "Genome Sequence of the plant pathogen Ralstonia solanacearum. Nature 415:497-502(2002).
          Pasteurella multocida.
Bacteria; Proteobacteria; Gam
Pasteurellaceae; Pasteurella.
NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome
SEQUENCE 200 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ralstonia solanacearum (Pseudomonas Bacteria; Proteobacteria; Betaprotec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21681879; PubMed=11823852;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probable histone
                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR005819; Histone_H5.
PRINTS; PR00624; HISTONEH5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ralstoniaceae; Ralstonia.
                                                            TOLA OR PM0968
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67; Conserv
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                                                                                                                                                                                             KKA 159
                                                                                                                                                                                                                    YEA 109
                                                                                                                                                                                                                                                                 АКЕЛАКАККЕЛУКЛЕАККУАКЛАК--ЛЕККЕУЛЛАЕЛККАЕЛАКАУКАЕ-ЛАКАЛАКЕЛА
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAKKQA-DADAKKAVEVAEKAAADAAEKKAAADAE-KKAAAAKKVAAAAEAKKKAAAEA
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                                                                                                                                                                                                                                            АКАККЕЛУКАЕЛККУАКАЛК-----ЛЕККЕУАЛАЕЛККАЕЛАК---ЛУКАЕЛАКАЛАКЕЛ
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                                                                                             (TrEMBLrel.
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                                                                                   17,
17,
22,
                                     Gammaproteobacteria;
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                                                                                                                                                                                                                                                                                                                                       Score 176.5; I
Pred. No. 3.2e
5; Mismatches
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                                                                                               sequence update)
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es 32;
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                                                                                   update)
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                                      Pasteurellales;
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RESULT 13
Q39576
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O61164

ID O6116

AC O6116

DT O1-AL

DT O1-AL

DT O1-BETYLT

GN MAEBI

OS Plasm

OX NCBI

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Best Local S
Matches 54
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Best Local (
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Proc. Natl. Acad. Sci. U.S.A. 95:1230-1235(1998).

EMBL; APO31886; AAC05366.1; -.

EMBL; APO31886; 199268 MW; EDA8E2DEFD87CE8
                                  Q39576;
Q39576;
01-NOV-1996
01-NOV-1996
01-MAR-2003
Histone H1.
                       Histone
CH1.
Chlamydomonas reinhardtii. Eukaryota; Viridiplantae; Chlorophyta;
                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium yoelii yoelii.
Eukaryota; Alveolata; Api
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01-OCT-2002
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01-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                      STRAIN=YM;
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                                             (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                    32.9%; Score 170.5; 53.5%; Pred. No. 0.0
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48.7%; Pred. No. 9.4
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                                             23,
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Chlorophyceae; Volvocales;
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RESULT 14
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Query Match
Best Local Similarity
Matches 54; Conserv
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Best Local :
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                                                                                                                                                                                                                                                                                                                                         O01395 PRELIMINARY; PRT;
O01395; PRELIMINARY;
O1-JUL-1997 (TrEMBLrel. 04, Created)
O1-JUL-1997 (TrEMBLrel. 04, Last seque)
O1-OCT-2002 (TrEMBLrel. 22, Last annot associated protein MST101(3))
MST101(3) OR DHMST101.
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ProDom; PD000373; Linkerhist N; 1.

SMART; SM00526; H15; 1.

SEQUENCE 232 AA; 24693 MW; 2D0
                                                                                                                                                                                                    Neesen J., Heinlein U.A.O., Buenemann H.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL
                                                    SEQUENCE
                                                                  Drosophila hydei (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musco
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR005818; Histone H1/H5
InterPro; IPR005819; Histone H5.
InterPro; IPR003216; Linkerhist N.
Pfam, PF00538; linker histone; I.
                                                                                                                                    -!- DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL EMBL; U85627; AAB51369.1; -.
                                                                                                                                                               -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                        NCBI_TaxID=7224;
                                                                                                                                                                                           SIMILARITY).
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                                                      275 AA;
 Conservative
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                                                      30436 MW;
           32.7%;
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 16;
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Score 169.5; DB 5;
Pred. No. 0.00013;
6; Mismatches 29;
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Pred. No. 0.0001;
0; Mismatches 3
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                                                       76BAA7B2A2DF732C CRC64;
                                                                                                                                                                                                                                                                                                                                                                    sequence update)
annotation update)
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                           Length
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Chlamydomonas
                            275;
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 13;
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AKKYAKKAEKAYAKK--AKAAKEKKAYAKKEAKAYKAAEAKKKAK-AEAKKYAKEAAKAK 57

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RESULT 15
Q3959
AC Q3959
AC Q3959
DT 01-NO
DT 01-NO
DT 01-OC
DB CGCR--
GN CGCR--
OS Chlam
OC Chlam
OC Chlam
OC Chlam
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Search completed: January 21, 2004, 09:00:27 Job time: 44.8831 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 31.6%; Score 164; DB 10; Length 265; Best Local Similarity 39.4%; Pred. No. 0.00029; Matches 50; Conservative 21; Mismatches 38; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92119224; PubMed=1731966;
Makarchuk W.W., Muller F.W., Beck C.F.;
"Two GC-rich DNA elements of Chlamydomonas reinhardtii with complex arrangements of directly repeated sequence motifs.";
Plant Mol. Biol. 18:143-146(1992).
EMBL; X17208; CAA35080.1; -.
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265 AA; 26216 MW; B35318B7377CF782 CRC64;
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
NCBI_TaxID=3055;
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Q39598; O1-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
CGCT-4 product (Fragment)
CGCR-4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB DB
519
312.5
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L: /SIDS1/gcgdata/g
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                  AAY82576
AAY82576
AAY82575
AAY82574
AAR06445
AAR06446
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AAY82573
AAY98499
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(without alignments)
330.323 Million cell updates/sec
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                 Copolymer molecula
Copolymer molecula
Recombinant copoly
Recombinant copoly
Copolymer molecula
Peptide #10 used i
                                                                                                                                                                                  Description
                                                                                                                           Copolymer molecula
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Peptide #8 used in	AAY98497	21	100	27.2	14
monocyto	91	23	239	.7	141.5
M. tuberculosis hi	AAY57353	21	214	7.	143
M. tuberculosis hi	AAY34055	20	214	7.	143
4 prote	ABP57088	24	452	7	143.5
(Lys)434 protein s	AAY56903	21	434	7.	144
Antibiotic potenti	AAW21591	18	434	7	144
lypept	AAW44829	18	111	7.	144
Drosophila melanog	ABB63276	22	299	8	Α.
Tumour neoangiogen	ABG71044	23	80	æ	•
Synthetic helical	AAR25206	13	140	æ	148.5
yoelii	AAB24128	21	1507	28.9	150
Drosophila melanog	ABB62173	22	607	9	151
ne Hi	AAY57331	21	222	9.	152.5
Human histone H1 i	AAY34033	20	222	9.	152.5
stone Hi	AAW29476	18	222	29.4	152.5
Haemophilus influe	ABG80418	23	372	29.6	153.5
histon	AAY76981	21	219	9	154
Human linker histo	AAE13237	23	130	9.	154.5
Peptide fragment o	AAU09945	23	130	29.8	154.5
Trypanosoma cruzi	AAR84565	16	564		157.5
芦	AAY57332	21	218	٥.	158
H1	AAY34034	20	218	30.4	158
æ	AAW29477	18	218	0	158
uzi	AAR84569	16	472	0	10
Human linker histo	AAE13234	23	234	0	159.5
Histone H1-4, frag	AAU09944	23	234		100
Human histone H1 i	AAY57358	21	226	0	•
Human histone H1 i	AAY34060	20	226		•
Human histone H1.5	AAY57366	21	158		60.
Ľ.	AAY34068	20	158	0	60.
æ	Φ	16	4	\vdash	on.
Amino acid sequenc	AAY14928	20	N	4	178
Pseudomonas aerugi	77	24		٠.	7
id tran	458	22	100	34.6	
Poly-Lys-Ala used	AAU04289	22	100	34.6	179.5

ALIGNMENTS

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RESULT 1
AAY82577
ID AAY8
XX AAY8
AC AAY8
XX AAY8
AC COpc
XX Oste
XX Oste
XX Oste
XX Infil
XW Infil
XW Infil
XW Hash
XX Pem
XX Oo-1
XX Copc
XX Copc
XX Oo-1
XX Oo-1
XX Oo-1
XX Oo-1
XX Oo-1
XX WO2C
XX Oo-1
XX VO2C
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antifilammatory; antidiabetic; thyronimetic; hamostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psori Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copolymer molecular weight TV-marker amino acid sequence SEQ ID
                                                                                                25-SEP-1998;
                                                                                                                                                                                                24-SEP-1999;
                                                                                                                                                                                                                                                                                                06-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified.
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     (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                           WO200018794-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pemphigus vulgaris;
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                                                                                                     98US-0101693.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lupus erythematosus
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Amino

acid polymer

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RESULT 2
AAY82576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cc and an amino acid composition corresponding to the compolymer. The glatiramer acetate related tetrapolymers. The polypeptides may also be cc used for treating and preventing immune diseases in a mammal. Autoimmune cd diseases which may be treated include either cell-mediated or creating and preventing immune diseases in a mammal. Autoimmune cd diseases which may be treated include either cell-mediated or cantibody-mediated diseases. Such diseases include arthritic conditions, cc multiple complianting diseases and inflammatory conditions, autoimmune haemolytic canaemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune cc uveoretinitis, Crohn's disease, chronic immune thyroidypaenia cc purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves cd disease, duillain-Barre's syndrome, Hashimoto's disease, idiopathic cmyxoedema, mysathenia gravis, psoriasis, pemphigus vulgaris, or systemic cc upus erythematosus. Mediated-mediated diseases which can be treated conclude host-versus-graft disease, graft-versus-host disease, and cc delayed-type hypersensitivity. The polypeptides of the invention have ce defined molecular weights and physical properties which are analogous to conclude with marvers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                 glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antinflammatory; antidiabetic; thromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis;
                Unidentified
                                                      pemphigus vulgaris;
                                                                             Hashimoto's disease; idiopathic myxoedema; myasthenia
                                                                                            Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;
                                                                                                                                                                                                                                        Copolymer; molecular weight marker; TV-marker; immune disease;
                                                                                                                                                                                                                                                                                Copolymer molecular weight TV-marker amino acid sequence SEQ ID
                                                                                                                                                                                                                                                                                                                        28-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                   AAY82576 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY82571 to AAY82577 represent specifically claimed copolymer molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 10; Page 14; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-317499/27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TEVA-) TEVA PHARM USA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        molecular weight markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                                                                                                                                                                                                                                   peptide;
                                                        systemic
                                                                                                                                                                                                                                                                                                                        entry)
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                                                        lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 519; D
Pred. No. 1.5
); Mismatches
                                                          erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21;
.5e-36;
g 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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                                                                             gravis;
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RESULT 3
AXY82575
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ID AXY8
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XX AXY8
XX COPO
XX COPO
XX COPO
XX COPO
XX OSTER
XW OSTER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC invention describes polypeptides (I) for determining the molecular weight cand an amino acid composition corresponding to the copolymer. The copolymer (CP), which has an identified molecular weight cand an amino acid composition corresponding to the copolymer. The copolymer act invention are used as molecular weight markers for composition are used as molecular weight markers for composition are used as molecular weight markers for continuous continuous and preventing immune diseases in a mammal. Autoimmune composition in the polypeptides may also be composed in the copolymers of the polypeptides may also be composed in the copolymers of the polypeptides may also be composed in the copolymers of the conditions, and the conditions of the copolities of the conditions, colletted diseases. Such diseases include arthritic conditions, codemyelinating diseases and inflammatory conditions, e.g. multiple considered in the copolymer conditions, colletted arthritis, autoimmune therefore the conditions, colletted arthritis, autoimmune thrombocytopaenia composed in the copolymers, collitis, contact sensitivity disease, diabetes mellitus, craves contact sensitivity disease, diabetes mellitus, craves considered include host-versus-graft disease, pand iseases, which can be treated conclude host-versus-graft disease, graft-versus-host disease, and conclude molecular weights and physical properties which are analogous to conclude the conditions of the invention have an actate molecules, which makes them ideal for use as
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                  Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprostepathic; immunosuppressive; antithyroid; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                           AAY82575 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 10; Page 14; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-SEP-1999;
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                                                                                                Copolymer molecular weight TV-marker amino acid sequence
                                                                                                                                            28-JUL-2000
                                                                                                                                                                                   AAY82575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             molecular weight markers
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(TEVA-) TEVA PHARM USA
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                                                                                                                                                                                                                                                                                                                             -KAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKKAYKAEAAKAAAKEAAYEA 86
                                                                                                                                                                                                                                                                                                                                                                                                          AKKYAKK-EKAYAKKA-----EKAAKKAEAKAYKAAEAKKKA------
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Pred. No. 2.2e-19;
1; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune upophoritis, autoimmune thyroiditis, autoimmune thyroiditis, cothoins disease, chronic immune thromboytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Gillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoddema, myasthenia gravis, posriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copolymer 1 related polypeptides used as glatiramer acetate and for treatment and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides [1] for determining the molecular weight of a copolymer (CP), which has an identified molecular weight
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(TEVA-)
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                                  AAY82574 standard; peptide; 66 AA
                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous glatiramer acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Page 14; 72pp;
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Pred. No. 1.8e-17;
1; Mismatches 3
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                                                                                                                                                                                                                                                                         include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypertides of the invention have defined molecular weights and physical properties which are analogous glatiramer acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
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                                                                                                                                                                                                                                                    molecular weight markers.
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TEVA PHARM
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USA INC.
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RESULT 5
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Matches 72
                                                                                                                                                                                              segments: YKK, EAE, KAK, AAK, and AAA. The N-terminal alanine real selft behind following CNBr cleavage of the fusion protein. The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control ademyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in
                                                                                                                                                                                                                                                                                       To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-77 were subcloned from pxRV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 US4691009, NRRL B-19810), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences. A methionine residue occurs between the Protein A and rCOP-1 sequences. Sequences, originating from the 5' linker sequence in order that the COP-1 polypeptide may be cleaved from the fusion protein. rCOP-1-77 contains oligonucleotide duplexes incoding the following segments: YKK, PAE, KAK, PAK, and PAA. The N-terminal alamine residue
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17-FEB-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Producing genes encoding random polymers of aminoacid(s) - for producing recombinant polypeptide(s) with biological and/or immunological activity
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See also AAQ05665.
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                            KKYAKKAEKA-----YAKKAKAAKEKKAYA----KKEAKAYKAAEA-----KKKAK-A 44
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                                                            Conservative
                                                                                                                                                    25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                copolymer 1-77, myelin basic protein analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (updated)
(first entry)
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89US-0312541.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
                                                                         40.3%;
                                                                                                                                                  correct
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                                                           8
                                                         Score 209; DB 11;
Pred. No. 1.9e-10;
8; Mismatches 20;
                                                                                                                                                    PA field.)
                                                                                       Length 154;
                                                            Indels
                                                            34;
                                                            Gaps
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RESULT 6
AAR06446
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                  demyelintis. They are used to prevent, arrest or demyelinating disorder, e.g. multiple sclerosis. They make used as additives to hair care products to confer ben effects on damaged hair or as supplements for diets defic see also AAQ05664.
(Updated on 25-MAR-2007
                                                                                                                                                            To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-19 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 US4691009, NRRL B-15910), a plasmid used to express protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences. A methionine residue occurs between the Protein A and rCOP-1 sequences, originating from the 5' linker sequence, in order that the COP-1 polypeptide may be cleaved from the fusion protein. rCOP-1-19 contains oligonucleotide duplexes incoding the following segments: YKX, ABZ, KAK, EKA, KCA, YEA, AKA KEA, and AAA. The N-terminal alanine residue is left behind following CNBr cleavage of the
                                                                                                                                                                                                                                                                                                                                                                                          producing genes encoding random polymers of aminoacid(s) - for producing recombinant polypeptide(s) with biological and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-FEB-1990;
17-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant copolymer 1; COP-1-19; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
03-JAN-1991
                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 12; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ06446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1990-255848/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cook KS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant copolymer 1-19, myelin basic protein analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR06446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR06446 standard; protein; 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                               immunological activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REPK ) REPLIGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KYKKEAEK--AKEA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AYKAEAAKAAAKEA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EYKKKAKAAAEAEYKKEAEEAEYKKYKKKAKKAKYKKKAKEAEKAKAAAEAEKAKEAEYK 141
106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (updated)
(first entry)
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89US-0312541.
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                                                                          diets deficient in
                                                                                        They may also
infer beneficial
                                                                                                                       control
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Query Match Best Local Similarity

36.0%; 55.0%;

Score 187; DB 11; Pred. No. 8.7e-09;

Length 106;

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AAY82573
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                                                                              and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Corbn's disease, chronic immune thromborytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; chronic immune thrombocytopaenia purpura; collitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxcedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY82573 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY82571 to AAY82577 represent specifically claimed copolymer molecul weight TV-marker polypeptides from the present invention. The present invention describes polypeptides [1] for determining the molecular weight of a copolymer (CP), which has an identified molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copolymer;
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                              myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris,
lupus erythematosus. Mediated-mediated diseases which can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 10; Page 14; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gad A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (YEDA ) YEDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TEVA-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKKYAKAAKAEKKEYAAAEAKKAEAA----KAYKAEAAKAAAK-EAAYE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKKAEKAYAKKAKAAKEKKAYAKKEAYKAEAKKKAKAEAKKYAKEAAKKAKKEAYKAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               molecular
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PHARM USA INC.
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                                  be treated
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                                                                or systemic
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The present invention relates to a transporter system for delivering CC nucleic acid to a cell. The system comprises a nucleic acid binding CC complex, consisting of a binding molecule bonded non-covalently to the CC binding molecule is spermine or a spermidine derivative. Nucleotide CC sequences AAA36633-A36652 and peptide sequences AAY98456-Y98500 are used in the construction of the transporter system of the invention. The CC transporter system is used in gene therapy, particularly to deliver nucleic acids to hepatocytes, muscle cells or bone forming cells, e.g. CC for treating cardiovascular disease, cancer, and infection. The CC transporter systems are also used to create transgenic animals (as models CC for human carcinogenesis or disease or for drug testing). Other uses CC include transforming cells to produce proteins, or transfecting cells in CC vitro to study the function of the nucleic acid. The use of a surface CC ingand allows specific targeting of selected cells and tissues. The lytic agent provides for release of the nucleic acid into the cellular CC interior, from endosomes, without requiring endosomal or lysosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transporter system; nucleic acid delivery; gene therapy; cancer; carcinogenesis; cardiovascular disease; infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              System for transporting nucleic acid into cells, useful e.g. in gene therapy and for generating transgenic animals, comprises binding agent linked to nucleic acid, surface ligand and lytic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAR-1992;
19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY98499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BAYU ) BAYLOR COLLEGE MEDICINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Column 125-128; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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93WO-US02725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93US-0167641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.8%;
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Pred. No. 1.6e-08;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----YKAEAAKAAAKEAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WOO SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
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delivering nucleic acid into a cell. The NTS contains but is not limited to 5 components: (a) the nucleic acid or a macromolecule to be delivered; (b) a molety that recognizes and binds to a cell surface receptor or antigen or is capable of entering a cell through cytosis; (c) a nucleic acid or macromolecular molecule binding moiety; (d) a molety that is capable of moving or initiating movement through a nuclear membrane; and/ or (e) a lysis molety that enables the transport of the entire complex from the cell surface directly into the cytoplasm of the cell. The NTS delivers nucleic acid into the cellular interior as well as the nucleus of specific cells. The NTS can be used to treat disorders by targeting specific nucleic acid accordingly. The NTS can also be used to create transgenic animals for assessing human disease, such as cancer, in an
                                                                                                                                                                                                                                                                                                                                                  14-DEC-1993;
20-MAR-1992;
19-MAR-1993;
                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                    Nucleic acid transport system, useful for creating transgenic for assessing human disease such as cancer in an animal model
                                                                                                                                                                                                                                                                                     WOO SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                  30-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid transport system; NTS; cell surface receptor; cytosi nuclear membrane; lysis moiety; transgenic animal; human disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY59044 standard;
                                                                                                                                                                The invention relates to a nucleic acid transport system (NTS)
                                                                                                                                                                                          Disclosure; Columns 123-124; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          03-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid delivery;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polymer seq ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                  93US-0167641.
92US-0855389.
93WO-US02725.
                                                                                                                                                                                                                                                                                                              COLLEGE MEDICINE
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                                                                                                                                                                                                                                                                                                                                          93US-0167641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Lys-Ala in
absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide;
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55.0%;
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                                                                                                                                                                                                                                                                                     Gottchalk S,
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Pred. No. 3.5
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                                                                                                                                                                                                                                                                                     Sparrow J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .5e-08;
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                                                                                                                                                                                                                                                                                     Smith
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14-DEC-1993; 20-MAR-1992; 19-MAR-1993;

93US-0167641. 92US-0855389. 93WO-US02725.

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SLC,

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Cristiano RJ,

Gottchalk S,

Sparrow

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(BAYU) BAYLOR COLLEGE MEDICINE

The sequence represents poly-Lys-Ala, used to bind nucleic acid in a nucleic acid transporter system. The nucleic acid transporter system uses nucleic acid binding complexes containing surface ligands which are capable of binding to a cell surface receptor and entering the cell through cytosis. The compounds of the invention are either ligands, binding molecules (surface ligands), lysis agents, spacer molecules or their intermediates. The ligands, binding molecules, lysis agents and spacer molecules are used in nucleic acid transporter systems to deliver nucleic acid into specific cells e.g. in gene therapy to deliver nucleic acid into hepatocytes, muscle cells or bone forming cells.

Nucleic acid transport system, useful for creating transgenic for assessing human disease such as cancer in an animal model

animals

Disclosure; Column 131; 111pp; English

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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 animal model. The NTS can be used in vitro with tissue culture cells which allows the role of various nucleic acids to be studied by targeting specific expression into specifically targeted tissue culture cells. The lysis agent within the NTS avoids the problem of endosomal/lysosomal
                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                               Nucleic acid transport; cytosis; ligand; lysis agent;
                                                                                                                                                                                                                                                                                                                                                                                                           AAU04289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                   05-JUN-1995;
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                                                                                                                                                                                                                                                                    US6177554-B1.
                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                        Poly-Lys-Ala
                                                                                                                                                                                                                                                                                                                                                                                                                          AAU04289 standard; Peptide; 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKAEKAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                         used in nucleic acid transporter system
                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                   95US-0462040
                                                                                                                                                                                                                                                                                           Location/Qualifiers
3..100
/note= "Lys-Ala in 1
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                                                                                                                                                                                                                                                                                     "Lys-Ala in
absent"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 179.5; DB (
Pred. No. 3.5e-08,
8; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                        spacer molecule;
                                                                                                                                                                                                                                                                                              be present
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                         This invention describes a novel system (I) for delivering a nucleic acid to a cell, comprising a binding complex comprising a ligand binding molecule noncovalently bound to a nucleic acid and covalently linked to a surface ligand, and a second binding complex comprising a second binding molecule noncovalently bound to a nucleic acid and covalently linked to a nuclear ligand. The complexes are simultaneously bound to the nucleic acid. The nucleic acid transporter system can also be used in a method for the in vivo targeting of the insertion of DNA into a cell. It can also be used in processes for producing transformed cell lines. The system can be used to deliver a variety or proteins and polypeptides, such as hormones, growth factors, enzymes, clotting factors, tumor suppressors, viral antigens, dargs, oncogenes, tumor antigens, tumor The transporter system uses lysis agents to overcome the problems of endosomal/lysosomal degradation seen with prior art systems.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-DEC-1993;
20-MAR-1992;
19-MAR-1993;
                                                                                                                                                                                                                                                                                                    Nucleic acid transporter system for delivering nucleic acid into a cell, useful for delivering proteins and polypeptides to cells, including growth factors, enzymes, hormones, and tumor suppressors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        growth factor; clotting factor; apolipoprotein; tumor antigen; tumor suppressor; viral antigen;
 Sequence
                                                                                                                                                                                                                                                                         Disclosure; Column 125-126; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bacterial antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid delivery; nucleic acid transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB45852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB45852 standard; Protein; 100
                                                                                                                                                                                                                                                                                                                                                                                                                             (BAYU ) BAYLOR COLLEGE MEDICINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid transporter system peptide ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   АККУАКА-АКАЕККЕУАААЕАККАЕААКАУКАЕААКАААК 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100
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                                                                                                                                                                                                                                                                                                                                                                                              Sparrow J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         93US-0167641.
92US-0855389.
93WO-US02725.
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Pred. No. 3.5e-08;
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                                                                                                                                                                                                                                                                                                                                                                                               Smith LC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         system; hormone; enzyme;
receptor; drug; oncogene
parasitic antigen;
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Query Match

Score 179.5;

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OKLEOQQVAAAKAAEQKKADEARKAEAQKAAEAKKADEAKKAAEAKAAEQKKQADIAKKR 158

АҮКАЕАККҮАКААКАЕККЕҮАААЕАККАЕЛАКАҮКАЕААКЛЛАКЕЛАҮЕА 109

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RESULT 12
ABJ18771
ID ABJ188
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                                                               Matches
                                                                                         Query Match
Best Local
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                                                                                                                                                                                                                      The invention comprises a method for identifying a compound capable of modulating biofilm formation by bacteria. The method of the invention is useful for identifying a compound capable of modulating biofilm formation by bacteria or modulating bacterial antibiotic resistance. The method of the invention is also useful for diagnosing and treating a subject (especially an immunocompromised human) that is afflicted with a biofilm-associated disease or disorder, such as: cystic fibrosis; AIDS; middle ear infections; acne; periodontal disease; catheter-associated infections; and medical device-associated infections. The present amino acid sequence represents a protein that is used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biofilm formation modulation; biofilm-associated disease; cystic fibrosis; AIDS; middle ear infection; acne; periodontal disease; catheter-associated infection; medical device-associated infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying compound capable of modulating biofilm bacteria/bacterial antibiotic resistance, useful for biofilm associated disease -
                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABJ18771 standard; Protein; 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 119-120; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-075601/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-APR-2001;
24-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-APR-2002; 2002WO-US12532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60
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                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNIV IOWA RES FOUND
KKAEKAYAKKAKAAKEK-----KAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKAEKAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    347 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aeruginosa biofilm formation-related
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                                                            Conservative
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2001US-344142P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                         34.5%;
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                                                                                         Score 179; DB 24;
Pred. No. 1.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 3.56
B; Mismatches
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smatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Greenberg EP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                   Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for treatment
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                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         formation
                                                                  10;
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                                                               Gaps
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                                                                                                                                                                                                                                                                                                       The invention provides heat-killed Mycobacterium vaccae, or recombinant CC M. vaccae proteins. The M. vaccae proteins may be employed to activate T cells and natural killer cells, to stimulate the production of CC cytckines, to enhance the expression of co-stimulatory molecules on CC and function. The proteins can be expressed by standard recombinant CC and function. The proteins can be expressed by standard recombinant CC methodology. Pharmaceutical compositions comprising the proteins or nucleic acid sequences encoding the proteins can be used for the CC treatment, prevention, and detection of disorders including infectious Cdleasses, immune disorders and cancer. In particular, the compounds and CC such as mycobacterial infections, asthma, allergies, tuberculosis, CC leprosy, sarcoidosis and lung cancers, and disorders of the skin such as gsoriasis, atopic dermatitis, eczema, allergic contact dermatitis, and skin cancers such as basal carcinoma, squamous cell
                                                                                                                  Query Match
Best Local S
Matches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-DEC-1997;
11-JUN-1998;
17-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 respiratory system; mycobacterial infection; allergy; tuberculosis; leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis; dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                  carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 239; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enhancing immune response to an antiger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-430163/36.
N-PSDB; AAZ11393.
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23-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          squamous cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of M. vaccae antigen GV-45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dendritic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-DEC-1997;
                                                                                                                                               Local Similarity
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                                                                                                                    60;
                                                             μ
     ARKAAKKAPAKKAAAKKAAPAKKAPAKKA-ATKAAPAKKATAAKKAAPAKKATAAKKAAP 170
                                              AKKYAKK--AEKAYAKKAKAAKB---KKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell maturation;
                                                                                                                                                                                                                                                                                        and melanoma.
                                                                                                                                                                                                                              223
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
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97US-0997362.
98US-0095855.
98US-0156181.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0205426.
97US-0996624.
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                                                                                                                                         34.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tan
                                                                                                                  6,
                                                                                                               Score 178; DB 20;
Pred. No. 1.1e-07;
6; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ָשׁ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immune
                                                                                                                                                                   Length 223;
                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorder; cancer;
                                                                                                                    10;
                                                                                                                  Gaps
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Conservative

18;

36;

Indels

11;

Gaps

445

AAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEA АККУАККАЕКАУАККАКААКЕККАУАККЕАКАУКААЕАКККАКАЕАККУА----КВААКА 56

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RESULT 14
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                                                                                                      AAR84565-R84569 are polypeptides of the TCR27 protein of T.cruzi
The proteins are all fusion products with glutathione-5-transferase
(GST) and some contain a linker sequence. The TCR27 protein comprises
a 95 amino acid (aa) N-terminal region; 69 repeats of a highly
conserved 14 as sequence and a 68 as C-terminal region. This sequence
encodes the GST sequence, the Ag44 polypeptide contg. 16 of the 69
repeat units and also contains the amino and carboxy terminal
peptides of TCR27. The TCR27 polypeptides of the invention are useful
for the diagnosis of CCR37 sequence (American Trypanosomiasis), they
are capable of detecting anti-T.cruzi antibodies; or for blood
screening. The TCR27 protein has epitopes to which most T.cruzi
infected individuals have antibodies. The TCR27 polypeptides will not
react with serum from patients with leishmaniasis, schistosomiasis,
corisionmune disease and are hence less likely to cause false
    Best Loc
Matches
                                Query Match
                                                                                                                                                                                                                                                                                                                                                                 New polypeptide(s) from the TCR27 protein of Trypanosoma cruzi - immunoassay reagent for specific diagnosis of Chagas disease, also related nucleic acid and transformed cells
                                                             Sequence
                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 40-41; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAT05332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCR27; Chagas disease; repeat unit; diagnosis; blood screening; recombinant; fusion protein; glutathione-S-transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR84568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR84568 standard; Protein; 643
                                                                                           positives
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-344618/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kirchhoff LV, Otsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KIRC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAR-1995;
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Local Similarity
les 52; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIRCHHOFF L
OTSU K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKKEAYKAEAKKYAKAAKAEKKEYA--AAEAKKAEAAKAYKAEAAKAAAK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in diagnosis.
                                                              .643 AA;
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/note= "16 of 69 repe
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                  31.3%;
    Score 162.5; DB 1
Pred. No. 6.5e-06;
8; Mismatches 36
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RESULT 15

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides a method for the diagnosis, prevention and CC treatment of ulcerative colitis (UC) using histone H1-like antigen, a govern antigen or a Bacteroides antigen as a target antigen. The novel method of diagnosing UC in a subject suspected of having inflammatory bowel disease (IBD) comprises: (1) obtaining a sample from the subject; (2) contacting the sample with a histone H1-like antigen, or perinuclear anti-neutrophil cytoplasmic antibody (pANCA)-reactive fragment, to form a complex of the histone H1-like antigen, or the pANCA-reactive fragment, and antibody to the histone H1-like antigen, or the pance of the complex of the complex where the presence of the complex complex where the presence of the complex complex is prevention and treatment of UC. The pance are useful in the complex porin antigen and Bacteroides antigen are useful in the complex diagnosis, prevention and treatment of UC. The methods can also be used for identifying agents useful for treating UC. The present sequence compressed to the complex useful for treatment of UC. The present sequence compressed to the complex useful for treatment of UC. The present sequence compressed to the complex useful for treatment of UC. The present sequence compressed to the complex useful for treatment of UC. The present sequence compressed to the complex useful for treatment of UC. The present sequence compressed to the complex useful for treatment of UC. The present sequence compressed to the complex useful for treatment of UC. The present sequence compressed to the complex useful for treatment of UC. The present sequence compressed to the complex useful for treatment of UC. The present sequence compressed to the complex useful for treatment of UC. The present sequence compressed to the complex useful for treatment of UC. The present sequence compressed to the complex useful for treatment of UC. The present sequence compressed to the complex useful for treatment of UC. The present sequence compressed to the complex useful for treatment of UC.
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Matches 51; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of histone H1, porin or Bacteroides antigens as targets for the diagnosis, prevention and treatment of ulcerative colitis
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                                                                                                                                                                                                                                                                                                                                                  51; Conservative
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                                                                                  АККЕЛУКАЕЛККУАКЛАКЛЕККЕУЛЛАЕЛККАЕЛЛКАУКЛЕЛЛКЛАЛКЕ 104
                                                                                                                                                                             AKPKAKKAGAAKAKKPAGATPKK--AKKAAGAKKAVKKTPKKAKKPAAAGVKKVAKSPKK 108
AKAAAKPKKATKSPAKPKAVKPKAAKPKAAKPKAAKPKAAKAKKAAAKK 157
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US-10-177-725-39	US-10-259-165-372	US-10-259-165-92	US-10-259-165-278	4	US-10-177-725-15	Ľ	US-10-177-725-41	US-10-177-725-19	US-10-229-567-2	US-10-229-567-13	US-10-229-567-14	US-10-177-725-45	US-10-229-567-1		US-10-128-714-3303	US-10-177-725-44	US-10-177-725-43	US-09-816-989A-2	US-10-029-386-32114	US-09-864-761-36182	US-10-156-761-10221	US-10-229-567-27	US-10-184-832-5	US-09-124-280A-3	US-09-820-843A-23	US-10-229-567-3	US-09-820-843A-8	US-09-820-843A-95	05-03-020-045W-74
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence		Sequence	Sequence	Sequence	Sequence			Sequence	Sequence 3	Sequence		Sequence	Sequence 3	Sequence	Sequence	Sequence	Sequence	ochrone
39, Appl	N	92, Appl		48, Appl	15, Appl	•	•	19, Appl	~	13, Appl	14, Appl	45, Appl		40, Appl	3303, Ap	44, Appl	43, Appl	2, Appli		36182, A	10221, A	27, Appl	5, Appli	-	23, Appl		8, Appli	95, Appl	+ Add: 12.7

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK TITLE OF INVENTION: AND FOR THERAPEUTIC USE FILE REPERENCE: 2609/60807-A-PCT-US CURRENT APPLICATION NUMBER: US/09/816,989A CURRENT FILING DATE: 2001-03-23 PRIOR APPLICATION NUMBER: 60/101,693 PRIOR APPLICATION NUMBER: 60/101,693 PRIOR FILING DATE: 1998-09-25 PRIOR FILING DATE: 1998-09-25 PRIOR FILING DATE: 1999-09-24 NUMBER: POT SEQ ID NOS: 7 SOFTWARE: Patentin version 3.1 SEQ ID NO 7 SEQ ID NOS: 7 SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                           Matches
                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/09816989A Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gad, Alexander APPLICANT: Lis, Doris
                                                                                                                                                                                                                                                                                                                                                      LENGTH: 109
TYPE: PRT
ORGANISM: Artificial Sequence
PPARTED.
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                                                                                                                                                                                           109;
61
                                             61 УКАЕАККУАКААКАЕККЕУАААЕАККАЕЛАКАУКАЕААКАЛАКЕЛАУЕА 109
                                                                                           1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 60
                                                                                                                       AKKYAKKAEKAYAKKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 60
YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA
                                                                                                                                                                                      100.0%; Score 519; DB 10; ilarity 100.0%; Pred. No. 1.9e-34; Conservative 0; Mismatches 0;
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                                                                             Query Match 55.7%;
Best Local Similarity 67.0%;
Matches 73; Conservative
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                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide -09-816-989A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Synthetic -09-816-989A-6
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APPLICANT: Lis, Doris
TITLE OF INVENTION: COPPLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT PPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARY TITLE OF INVENTION: AND FOR THERAPEUTIC USE FILE REFERENCE: 2609/60807-A-PCT-US CURRENT APPLICATION NUMBER: US/09/816,989A CURRENT FILING DATE: 2001-03-23
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NUMBER OF SEQ ID NOS: 7
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PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                              FEATURE:
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                                                                                                                                                                                                                                                        TYPE: PRT
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                          AKKYAKKAEKAYAKKAAKAAKEKKAYAKKEAKAYKAABAKKKAKAEAKKYAKEAAKAKKEA 60
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  AKKYAKK-EKAYAKKA-----EKAAKKAEAKAYKAAEAKKKA-
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Pred. No. 3.2e
1; Mismatches
                                                                           Score 289; DB 10;
Pred. No. 2.1e-16;
1; Mismatches 3
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                                                                                                                       DB 10;
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                                                                                                                     Length 77;
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                                                                               Gaps
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36
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; FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-3
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US-09-816-989A-4
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                                                                                                                                                SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 56
TYPE: PRT
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
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APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
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TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT PAPALICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                   TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES 1
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
RRIOR APPLICATION NUMBER: 60/101,693
RRIOR PILING DATE: 1998-09-25
PRIOR PILING DATE: 1998-09-24
PRIOR FILING DATE: 1998-09-24
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                                                                                                                            ORGANISM: Artificial Sequence
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TYPE: PRT
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34.8%;
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Pred. No. 1.1e-11;
  Score 180.5; DB 10;
Pred. No. 5.8e-08;
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                    Length 56;
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; TYPE: PRT ; ORGANISM: Mycobacterium vaccae US-10-205-979-52
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; ORGANISM: Pseudomonas aeruginosa
US-10-127-032-120
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                                                          SEQ ID NO 52
LENGTH: 223
                                                                                                                                                                                                                                                                                                                                                                          Sequence 52, Application US/102 Publication No. US20030147861A1
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Best Local Similarity
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                                                                                                CURRENT APPLICATION NUMBER: US/10/205,979
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/308,446
PRIOR FILING DATE: 2001-07-26
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: US 60/344,142
PRIOR FILING DATE: 2001-10-24
NUMBER OF SEO ID NOS: 170
                                                                                                                                                                                                                          TITLE OF INVENTION: Compounds and Methods for the Modulation TITLE OF INVENTION: of Immune Responses FILE REFERENCE: 11000.1063U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Greenberg, Everett Peter
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION
TITLE OF INVENTION: BIOFILM FORMATION
FILE REFERENCE: UIZ-070CP
                                                                                                                                                                                                                                                                                         APPLICANT: Watson, James D. APPLICANT: Tan, Paul L. J. APPLICANT: Abernethy, Nevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/127,032
CURRENT FILING DATE: 2002-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Whiteley, Marvin APPLICANT: Bangera, M. Gita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH: 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lence 120, A
lication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 A-EDEAKK--KAAEDAKKK-AAEDAKKKAAEEAKKKAAAEAAKKKAAVEA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 АУКАЕАККҮАКААКАЕККЕУАЛАЕАККАЕЛАКАУКАЕЛАКАЛАКЕЛАУЕЛ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 OKLEQQQVAAAKAAEQKKADEARKAEAQKAAEAKKADEAKKAAEAKAAEQKKQADIAKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 ККАЕКАУАККАКААКЕК-----КАУАККЕАКАУКААЕАКККАКАЕАККУАКЕААКАККЕ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         Application US/10205979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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 Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YKAEAAKAAAKEAAYEA 56
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; ORGANISM: Mycobacterium vaccae
US-10-051-643-201
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 201
LENGTH: 223
                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                          Sequence 9889, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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Publication No. US20020197265A1
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Matches (
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                                                                                                                                      Matches
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                                                                                                                                                                                                                                             APPLICANT:
                               CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                  APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 08/996,624 PRIOR FILING DATE: 1997-12-23 NUMBER OF SEQ ID NOS: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 11000.1008c2
CURRENT APPLICATION NUMBER: US/10/051,643
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US09/156,181
PRIOR FILING DATE: 1998-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Watson, James D. APPLICANT: Tan, Paul L. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
TITLE OF INVENTION: System using Mycobacterium Vaccae
NUMBER OF SEQ ID NOS: 15109
EQ ID NO 9889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 AKKEAYKAEAKKYAKAAKAEKKEYA--AAEAKKAEAAKAYKAEAAKAAAK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 AKKEAYKAEAKKYAKAAKAEKKEYA--AAEAKKAEAAKAYKAEAAKAAAK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYAKK--AEKAYAKKAKAAKE---KKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 АККҮАКК--АЕКАҮАККАКААКЕ---ККАҮАККЕАКАҮКААЕАКККАКАЕАККҮАКЕААК 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARKAAKKAPAKKAAAKKAAPAKKAPAKKA-ATKAAPAKKATAAKKAAPAKKATAAKKAAP 170
                                                                                                                                                                                                                                               ISHIKAWA, JUN
HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.3%;
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54.5#;
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Pred. No. 3.8e-07;
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Pred. No. 3.8e-07
5; Mismatches 3
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RESULT 11
US-10-229-567-40
; Sequence 40, Application US/10229567
; Publication No. US20030092080A1
; GENERAL INFORMATION:
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Publication No. US2003003963A1

GENERAL INFORMATION:
APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: Q63915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.0
SEQ ID NO 27
LENGTH: 356
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Best Local Similarity
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Best Local Similarity
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
OTHER INFORMATION: gi|9656364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
OTHER INFORMATION: tola protein
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                                                                        APPLICANT: Braun, Jonathan
Cohavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
Ulcerative Colitis, and Clinical Subtypes
Microbial UC pANCA antigens
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305
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                                                                                                                                                                                                                                                                                                                                                                                                                                             57 KKEAYKAEAKKYAK------AAKAEK----KEYAAAEAKKAEAAKAYKAEAAKA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 АҮКАЕАККҮАКААКАЕККЕҮАААЕАККАЕААКАҮКАЕААКАААКЕАА 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48;
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                                                                                                                                                                                                                                                                                                                             EAERKAQEA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAAREAEKLREQKEQERLAAEQKAREEKERAAKAEAERKVKEEAAKKAEQERVAKEAAAA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKKAAAKKSAPAKKSAPGKTAAKKAAAKKTAPAKKSAAKKSAAKKTA 351
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44.9%; Pred. No. 9.9e-06;
ative 15; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 356;
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RESULT 12
US-10-229-567-32
; Sequence 32, Application Us,...
; Publication No. US20030092080A1
; GENERAL INFORMATION:
    APPLICANT: Braun, Jonathan Cohavy, Offer
    TNVENTION: Diagnosi
    Ulcerat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-229-567-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 40: SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/229,567
FILING DATE: 27-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 30.9%;
Local Similarity 46.8%;
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PILING DATE: «Unknown»
APPLICATION NUMBER: US 09/041,889
PILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Diagnosis, Prevention and Treatment Ulcerative Colitis, and Clinical Sul Microbial UC panch antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 АККУАККАЕКАУАККАКААКЕККАУАККЕАКАУКАА----ЕАКККАКАЕАККУАКЕААК 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/10/229,567
FILING DATE: 27-Aug-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKAAAKPKKATKSPAKPKAVKPKAAKPKAAKPKAAKPKAAKAKKAAAKK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          АККЕАУКАЕАККУАКААКАЕККЕУАЛАЕАККАЕЛАКАУКАЕЛАКАЛАКЕ 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKPKAKKAGAAKAKKPAGATPKK--AKKAAGAKKAVKKTPKKAKKPAAAGVKKVAKSPKK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Diego
STATE: California
                                                                                                                                                                                                                             CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/10229567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 158 amino acids
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Pred. No. 6.4e-06;
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LENGTH: 226 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-229-567-32
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US-10-262-209-1
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Best Local Similarity 46.8%;
Matches 51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10262209
Publication No. US20030125239A1
                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1
                                                                                                                                                                                                                                                            -10-262-209-1
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: UK 0218324.2
PRIOR PILING DATE: 2002-08-07
PRIOR PELICATION NUMBER: PCT/GB01/01699
PRIOR PILING DATE: 2001-04-12
PRIOR PILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: UK 0102667.3
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: UK 0009080.3
                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/262,209
CURRENT FILING DATE: 2002-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Esseghir, Selma
TITLE OF INVENTION: Compositions for Drug Delivery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Crisanti, Andrea
APPLICANT: Esseghir, Selma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: GJE-6703
                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                        ENGTH: 234
                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/417,264
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: US 09/041,889
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
167
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                                                                                       109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 АККЕЛҮКЛЕЛККҮЛКЛАКЛЕККЕҮЛЛАЕЛККАЕЛАКАҮКЛЕЛАКЛАЛКЕ 104
                                          60 АУКАЕАККҮАКААКАЕККЕҮАААЕАК-----КАЕААКАҮКАЕААКАААКЕААҮЕ 108
                                                                                                                                                                         53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: <Unknown>
  AKKAKSPKKAKAAKPKKAPKSPAKAKAVKPKAAKPKTAKPKAAKPKKAAAKKKKLE 222
                                                                                    KKAASGEAKPKAKKAGAAKAKKPAGAAKKPKKATGAATPKKSAKKTPKKAKKPAAAA--G
                                                                                                                          ККҮАККАЕКАҮАККАКАКККК--АУАККЕАКАҮКААЕАКККАКАЕАККҮАКЕААККЕ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKAAAKPKKATKSPAKPKAVKPKAAKPKAAKPKAAKPKAAKKAAAKK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
                                                                                                                                                                         Conservative
                                                                                                                                                                                           30.7%;
45.7%;
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Pred. No. 9.3e-06;
                                                                                                                                                                                         Score 159.5; DB 1
Pred. No. 1.2e-05;
                                                                                                                                                                         Mismatches
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                                                                                                                                                                       Indels
                                                                                                                                                                                                             Length
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US-10-229-567-4
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                                                                                                                                                                                                                                                     , SEQUENCE DESCRIPTION: SEQ ID NO: US-10-229-567-4
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                                                                                                                                                                  Query Match
Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/417,264
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: US 09/041,889
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATB: US/10/229,567
FILING DATE: 27-Aug-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Diagnosis, Prevention and Treatment of Ulcerative Colitis, and Clinical Subtypes Thereof, Using Microbial UC pANCA antigens
                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Braun, Jonathan
Cohavy, Offer
                                                                                    108 KKAASGEAKPKAKKAGAAKAKKPAGAAKKPKKATGAATPKKSAKKTPKKAKKPAAAA--G 165
166 AKKAKSPKKAKAAKPKKAPKSPAKAKAVKPKAAKPKTAKPKAAKPKKAA 214
                                        60 АУКАЕАККУАКААКАЕК--КЕУААЛЕАККАЕЛАКАУКАЕЛАКАЛАКЕЛА 106
                                                                                                                              N
                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
LOCATION:
                                                                                                                          ККУАККАЕКАУАККАКАКАККК--АУАККЕАКАУКААЕАКККАКАЕАККУАКЕААКАККЕ 59
                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
H1-S-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 218 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Campbell & Flores LLP STREET: 4370 La Jolla Village Drive, Suite
                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (619)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
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1..218
                                                                                                                                                                                        30.4%;
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                                                                                                                                                                    Score 158; DB 15;
Pred. No. 1.4e-05;
7; Mismatches 43
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                                                                                                                                                                         43;
                                                                                                                                                                                                               Length 218;
                                                                                                                                                                         Indels
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RESULT 15 US-10-262-209-2

Sequence 2, Application US/10262209
Publication No. US20030125239A1
GENERAL INFORMATION:
APPLICANT: Crisanti, Andrea

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Page 6
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TITLE OF INVENTION: Compositions for Drug Delivery
FILE REFERENCE: GJE-6703
CURRENT APPLICATION NUMBER: US/10/262,209
CURRENT PAILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: UK 0218324.2
PRIOR FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: PCT/GB01/01699
PRIOR FILING DATE: 2001-04-12
PRIOR PLICATION NUMBER: UK 0102667.3
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-03
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-03-03
PRIOR FILING DATE: 2001-03-03
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 130
TYPE: PAT
ORGANISM: Homo sapiens
US-10-262-209-2
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                                                                                                                                                                                         Query Match 29.8%; Score 154.5; DB 15; Length 130; Best Local Similarity 47.3%; Pred. No. 1.6e-05; Matches 52; Conservative 8; Mismatches 43; Indels 7; Gaps
                         17 KKAASGEAKPKAKKAGAAKAAKKPAGAAKKPKKATGAATPKKSAKKTPKKAKKPAAAA-- 74
2 KKYAKKAEKAYAKK---AKAAKEKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKK 58
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Search completed: January 21, 2004, 09:10:08 Job time: 39.6364 secs

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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GenCore version (c) 1993 - 2004
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US-08-406-890A-64
US-08-460-890A-64
US-08-460-971A-64
US-08-462-040-64
US-08-426-040-64
US-09-252-991A-29581
US-09-255-426-201
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US-09-328-352-5321
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Compugen Ltd
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32, Appl
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110, Appl
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CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 199-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 109
TYPE: PRT
ORGANISM: Artificial Sequence

OTHER INFORMATION: OTHER INFORMATION:

Description of Artificial Sequence: PEPTIDE

SYNTHETIC

FEATURE:

ALIGNMENTS

RESULT 1 US-09-405-743A-7

Sequence 7, Application US/09405743A
Patent No. 6514938
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A

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                                                                                       GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
                                                NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Ve
SEQ ID NO 6
                                                                                                                                                                                               Sequence 6, Application US/09405743A Patent No. 6514938
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 109;
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Best Local Similarity
TYPE: PRT ORGANISM: Artificial Sequence
                                  LENGTH:
                                                                                                                                                                                                                                                                                                  62
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                                  86
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                                                                   Ver. 2.1
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Pred. No. 4.7e-37;
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; OTHER INFORMATION: Description of Artificial Sequence: ; OTHER INFORMATION: PEPTIDE US-09-405-743A-4
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US-09-405-743A-4
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OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: PEPTIDE
US-09:405-743A-6
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Patent No. 6514938
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
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LENGTH: 77
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Best Local Similarity
                                                                                                                 SOFTWARE:
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FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                    FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
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                                                ORGANISM: Artificial Sequence FEATURE:
                                                                                   LENGTH: 66
TYPE: PRT
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TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 АККУАККАЕКАУАККАКААКЕККАУАККЕАКАУКААЕАКККАКАЕАККУАКЕААКАККЕА 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                       PatentIn
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Pred. No. 6.5e-20;
1; Mismatches 3
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Pred. No. 5.4e-18;
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RESULT 6
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OTHER INFORMATION:
US-09-405-743A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09405743A
Patent No. 6514938
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Woo, Sa
APPLICANT: Smith,
APPLICANT: Cristia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local Similarity 45.9%;
                                                                                                                                                                                                                                                                                                                                      Patent No. 5994109
                                                                                                                                                                                                                                                                                                                                                  Sequence 64, Application US/08460890A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 60807-A.
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 56
                                         COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                 ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth S
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                             APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: MUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
              COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.O
 SOFTWARE:
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                                                                                                                                                                                                                                                                                           Smith, Louis C.
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SYSTEM: IBM P.C. DOS 5. FastSEQ for Windows 2.0
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               .C. DOS 5.0
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Pred. No. 5.2e-13;
0; Mismatches 4;
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Pred. No. 4.5e-09;
3; Mismatches 3
                                                             1.44 Mb
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08, FILING DATE: June 5, 1995

US/08/460,890A

CLASSIFICATION:

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                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6033884
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 67-3510
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                         NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 631 West 700
                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NUCLEIC ACID TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
OTHER INFORMATION: "Lys Ala" in positions 3 to
OTHER INFORMATION: present or absent.
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APPLICATION NUMBER:
                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              APPLICANT: Cristiano, Richard J. APPLICANT: Gottchalk, Stephen
                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/07
FILING DATE: March 19, 1993
                                              OPERATING SYSTEM:
SOFTWARE: FastSE(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,3
                                                                                                                                                COUNTRY: U.S.A. ZIP: 90071-2066
                                                                                                                                                                                              CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH:
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Smith, Louis C.
                                            SYSTEM: IBM P.C. DOS 5.0
FastSEQ for Windows 2.0
                                                                         IBM Compatible
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December 14, 1993
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             US/08/167,641C
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Pred. No. 9.7e-09;
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                                                             DOS 5.0
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (213) 955-044
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,9711
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APPLICATION NUMBER: 07/855,389

FILING DATE: MARCH 20, 1992

APPLICATION NUMBER: PCT/US93/02725

FILING DATE: MARCH 19, 1993

ATTORNEY/AGENT INFORMATION:
       FILING DATE: June 5, 1972
FILING DATE: June 5, 1972
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PARTICL NUMBER: 08/167,641
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
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LENGTH: 100 amino acids
                                                                                                                                                                                    ZIE: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NUCLEIC ACID TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: "Lys Ala" in positions 3 to OTHER INFORMATION: present or absent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 АККҮАКА-АКАЕККЕУЛАЛЕЛККАЕЛАКАҮКАЕЛАКАЛАК 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55;
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December 14,
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55.0%;
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                                                                                                                                                    IBM P.C. DOS 5.0
                                                                                           US/08/460,971A
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Pred. No. 9.7e-09;
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REGISTRATION NUMBER: 32,327
REFERENCE, DOCKET NUMBER: 212/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELERAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS TITLE OF INVENTION: METHODS OF USE NUMBER OF SEQUENCES: 65 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: WOO, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
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LENGTH: 100 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US9:
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                      CLASSIFICATION: 536 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: June 5, 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20,1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19,1993
                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                          COMPUTER: IBM CON
OPERATING SYSTEM:
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STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A
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6177554
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UMBER: PCT/US93/02725
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                                                                                        08/167,641
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Pred. No. 9.7e-09;
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US-09-252-991A-29581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-252-991A-29581
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                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29581
LENGTH: 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity 55.0%;
                                                                                                                                                   Matches
                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (213) 955-0444
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                               TYPE: PRT
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LENGTH: 100 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZLECUPANE: (213)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                 Match 34.5%; Score 179; DB 4; Local Similarity 49.1%; Pred. No. 4.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
219 A-EDEAKK--KAAEDAKKK-AAEDAKKKAAEEAKKKAAAEAAKKKAAVEA 264
                                                                        159 QKLEQQQVAAAKAAEQKKADEARKAEAQKAAEAKKADEAKKAAEAKAAEQKKQADTAKKR
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                                                                                                           6 ККАЕКАУАККАКАКАКЕК-----КАУАККЕАКАУКААЕАКККАКАЕАККУАКЕААКАККЕ 59
                                  АУКАБАККУАКААКАЕККЕУАААБАККАБААКАУКАБААКАААКБААУБА 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           АККҮАКА-АКАЕККЕҮАААЕАККАЕААКАҮКАЕААКААК 103
                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09252991A
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Pred. No. 9.7e-09;
                                                                                                                                                   Mismatches
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                                                                                                                                                                                      Length 407;
                                                                                                                                                   Indels 10;
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RESULT 11 US-09-095-855-201

Sequence 201, Application US/09095855 Patent No. 6160093 GENERAL INFORMATION:

APPLICANT:

Tan, Paul

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RESULT 12
US-09-205-426-201
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US-09-095-855-201
                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                       Sequence 201, Application US/09205426 Patent No. 6406704
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Compounds and Methods for Treatment and
TITLE OF INVENTION: Diagnosis of Mycobacterial infections
FILE REFERENCE: 11000.1002c4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION NUMBER: US/09/205,426
CURRENT FILING DATE: 1998-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705
PILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873
FILING DATE: 12-UUN-1997
APPLICATION NUMBER: 08/997
FILING DATE: 23-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
OPERATING SYSTEM: DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Sleath, Janet REGISTRATION NUMBER: 37,007 REFERENCE/DOCKET NUMBER: 111 TELECOMMUNICATION INFORMATION: TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/095,855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Visser, Eli
APPLICANT: Skinner, Ma
APPLICANT: Prestidge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: Sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                           112 АККАЛККАРАККАЛАККАЛРАККАРАККА-АТКАЛРАККАТАЛККАЛРАККАТЛАККАЛР 170
                                                                                                                                                                                                                                                                                                                56 АККЕЛҮКАЕЛККҮАКЛАКЛЕККЕҮЛ--ДЛЕЛККАЕЛЛКАЕЛЛКАЕЛЛКАЛАК 103
                                                                                                                                                                                                                                                                                                                                                                                                                                    60;
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Skinner, Margot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Law Offices of Ann W. Speckman
01 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 178; DB 3;
Pred. No. 2.9e-08;
6; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11000.1002c3
                                                                                                                                                                                                                                                                                                                                                                                                                                  34; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 223;
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; MOLECULE TYPE: protein US-08-216-894-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mycobacterium vaccae US-09-205-426-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Appli
Patent No. 587673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 201
LENGTH: 223
Matches
                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local (
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EARLIER FILING DATE: 1996-08-29
EARLIER FILING DATE: 1996-08-29
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER FILING DATE: 1998-06-11
EARLIER APPLICATION NUMBER: 08/997,362
EARLIER FILING DATE: 1997-12-23
EARLIER APPLICATION NUMBER: 08/873,970
                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
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                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 643 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                NAME: BENT, Stephen A.
REGISTATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,894
FILING DATE: 24-MAR-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kirchhoff, Louis V.
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                              TELEFAX: 12.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 3000
CTTY: Washington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 АККЕЛУКЛЕЛККҮАКЛАКЛЕККЕҮЛ--ЛЛЕЛККАЕЛЛКАУКЛЕЛАКАЛАК 103
52,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08216894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Foley & Lardner
3000 K Street, N.W., Suite 500
lashington, D.C.
                                                                                                                                                                                                                                (202) 672-5399
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.3%;
                  31.3%; Score 162.5; DB 2 44.4%; Pred. No. 1.6e-06;
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  18;
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                                                                                                                                                                                                                                                                                           85326/102/DRLO
  Mismatches
                                    DB 2;
  36;
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Indels 11;
                                    Length
                                      643;
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US-09-115-746-8
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; MOLECULE TYPE:
US-09-115-746-8
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                                                                                                                            US-09-041-889-40
                                                                                                                                              RESULT 15
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Best Local S
Matches 52
                                                                      Sequence 40, Applicat Patent No. 6033864 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Braun, Jonathan APPLICANT: Cohavy, Offer TITLE OF INVENTION: Diagnos TITLE OF INVENTION: Ulcerat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Otbu, Keiko
TITLE OP INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
PRIOR APPLICATION NUMBER: '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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                                                                                                                                                                                                505 TKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEAA 561
                                                                                                                                                                                                                                                                       445 AAEATKVAEAEKOKAAEATKVAEAEKOKAAEATKVAEAEKOKAAEATKVAEAEKOKAAEA 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57
                                                                                                                                                                                                                     57 KK--EAYKAEAKKYAKAAKAEKKEYA----AAEAKKAEAAKAYK-AEAAKAAAKEAA 106
                                                                                                                                                                                                                                                                                             1 AKKYAKKAEKAYAKKAAKEKKAYAKKEAKAYKAAEAKKKAAKAEAKKYA----KEAAKA 56
                                                                                       0, Application US/09041889
6033864
                                                                                                                                                                                                                                                                                                                                          Similarity 44.4
52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20007-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEAA 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KK--EAYKAEAKKYAKAAKAEKKEYA----AAEAKKAEAAKAYK-AEAAKAAAKEAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               643 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Foley & Lardner
3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : (202)672-5300
(202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kirchhoff, Louis V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -5109
                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                          31.3%; Score 162.5; DB 3;
44.4%; Pred. No. 1.6e-06;
ative 18; Mismatches 36;
 Diagnosis, Prevention and Treatment of Ulcerative Colitis, and Clinical Subtypes Thereof, Using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08/216,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85326/102/DRLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suite 500
                                                                                                                                                                                                                                                                                                                                                                           Length 643;
                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                           11,
                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                          Query Match
                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A
REGISTRATION NUMBER: 31,8
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acid
                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                               TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Diego
STATE: California
                                                                                                                30.9%;
Local Similarity 46.8%;
es 51; Conservative
                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
109
                                                               51
                               56
 АКАДАКРККАТКЅРАКРКАЧКРКААКРКААКРКААКРКААКАККАЛАКК 157
                              АККЕАУКАЕАККУАКААКАЕККЕУАЛАЕАККАЕЛАКАУКАЕЛАКАЛАКЕ 104
                                                               AKPKAKKAGAAKAKKPAGATPKK--AKKAAGAKKAVKKTPKKAKKPAAAGVKKVAKSPKK 108
                                                                                            АККУАККАЕКАУАККАКААКЕККАУАККЕАКАУКАА----ЕАКККАКАЕАККУАКЕААК 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                          (619)
                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                          535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Microbial UC pANCA antigens
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                                                                                                                                                                                                                                                                                           40:
                                                                                                                                                                                                                                                                                                                                                                                                                                      08/837,058
                                                                                                                                                                                                                                                                                                                                                            P-PM
                                                                                                                            Score 160.5; DB 3
Pred. No. 5.9e-07;
7; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                            3006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Version
                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #1.25
                                                                                                                               44;
                                                                                                                               Indels
                                                                                                                                                             Length
                                                                                                                                                               158;
                                                                                                                               7;
                                                                                                                               Gaps
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Search completed: January 21, 2004, 09:02:21 Job time: 21.526 secs